









QY 890 AAGAAATCCAAATACCCGCGCTCTACCTGTTTGGATCAGAGTTTGGAAATCTGTCA 949  
 Db 914 AAGAAATCCAAATACCCGCGCTCTACCTGTTTGGATCAGAGTTTGGAAATCTGTCA 973  
 QY 950 TTCAACACACAGCTTCCAAATGATGTCGTAATGTTTACCAACACAGCTTCCGAGTTCGAT 1009  
 Db 974 TTCAACACACAGCTTCCAAATGATGTCGTAATGTTTACCAACACAGCTTCCGAGTTCGAT 1033  
 QY 1010 GTGAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1069  
 Db 1034 GTGAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093  
 QY 1070 AAGGCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1129  
 Db 1094 AAGGCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153  
 QY 1130 CCAAAATAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189  
 Db 1154 CCAAAATAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1213  
 QY 1190 TTGTATGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249  
 Db 1214 TTGTATGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1273  
 QY 1250 AAATGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309  
 Db 1274 AAATGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1333  
 QY 1310 GGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369  
 Db 1334 GGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1393  
 QY 1370 ATCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429  
 Db 1394 ATCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1453  
 QY 1430 GTAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1489  
 Db 1454 GTAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1513  
 QY 1490 TTTTCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1549  
 Db 1514 TTTTCAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573  
 QY 1550 CTAAATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609  
 Db 1574 CTAAATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1633  
 QY 1610 GTTCTGAT 1669  
 Db 1634 GTTCTGAT 1693  
 QY 1670 AAGAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1729  
 Db 1694 AAGAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1753  
 QY 1730 ATATGAT 1789  
 Db 1754 ATATGAT 1813  
 QY 1790 AATGAT 1849  
 Db 1814 AATGAT 1886

RESULT 4  
 AR055003 3633 bp mRNA linear PRI 25-JAN-2002  
 LOCUS Homo sapiens LATA3 mRNA for system A amino acid transporter 3,  
 DEFINITION complete cds.  
 AR055003  
 ACCESSION AR055003.1 GI:18369788

KEYWORDS  
 SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

FASTA

ORIGIN

Query Match

Best Local Similarity

Matches 1646

Conservative

Mismatches

4

Models

0

Gaps

0

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

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QY

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QY

Db

QY

Db





[illegible]





















GenCore version 5.1.3  
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GM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 08:33:36 ; Search time 1293.47 Seconds  
(without alignments)  
11249.881 Million cell updates/sec

Title: US-09-776-705-3-copy\_1\_500

Perfect score: 500

Sequence: 1 agcttagcaatagatgacaa.....ataatgcacaaataaactgaa 500

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2051640 seqs, 1155102078 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 27666600

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenBank

2: gb\_fa:

3: gb\_hq:

4: gb\_in:

5: gb\_em:

6: gb\_ov:

7: gb\_fa:

8: gb\_fa:

9: gb\_fa:

10: gb\_fa:

11: gb\_fa:

12: gb\_fa:

13: gb\_fa:

14: gb\_fa:

15: gb\_fa:

16: gb\_fa:

17: gb\_fa:

18: gb\_fa:

19: gb\_fa:

20: gb\_fa:

21: gb\_fa:

22: gb\_fa:

23: gb\_fa:

24: gb\_fa:

25: gb\_fa:

26: gb\_fa:

27: gb\_fa:

28: gb\_fa:

29: gb\_fa:

30: gb\_fa:

31: gb\_fa:

32: gb\_fa:

33: gb\_fa:

34: gb\_fa:

35: gb\_fa:

36: gb\_fa:

37: gb\_fa:

38: gb\_fa:

39: gb\_fa:

40: gb\_fa:

41: gb\_fa:

Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500	100.0	37921	9	AC005854 Homo sapi
2	500	100.0	37921	9	AC008014 Homo sapi
3	492	97.4	37921	2	AC008014 Homo sapi
4	492	97.4	37921	2	AC008014 Homo sapi
5	492	97.4	37921	2	AC008014 Homo sapi
6	492	97.4	37921	2	AC008014 Homo sapi
7	492	97.4	37921	2	AC008014 Homo sapi
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12	492	97.4	37921	2	AC008014 Homo sapi
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40	492	97.4	37921	2	AC008014 Homo sapi
41	492	97.4	37921	2	AC008014 Homo sapi

# ALIGNMENTS

Result	Score	Query Match	Length	DB ID	Description
1	500	100.0	37921	9	AC005854 Homo sapi
2	500	100.0	37921	9	AC008014 Homo sapi
3	492	97.4	37921	2	AC008014 Homo sapi
4	492	97.4	37921	2	AC008014 Homo sapi
5	492	97.4	37921	2	AC008014 Homo sapi
6	492	97.4	37921	2	AC008014 Homo sapi
7	492	97.4	37921	2	AC008014 Homo sapi
8	492	97.4	37921	2	AC008014 Homo sapi
9	492	97.4	37921	2	AC008014 Homo sapi
10	492	97.4	37921	2	AC008014 Homo sapi
11	492	97.4	37921	2	AC008014 Homo sapi
12	492	97.4	37921	2	AC008014 Homo sapi
13	492	97.4	37921	2	AC008014 Homo sapi
14	492	97.4	37921	2	AC008014 Homo sapi
15	492	97.4	37921	2	AC008014 Homo sapi
16	492	97.4	37921	2	AC008014 Homo sapi
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19	492	97.4	37921	2	AC008014 Homo sapi
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22	492	97.4	37921	2	AC008014 Homo sapi
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26	492	97.4	37921	2	AC008014 Homo sapi
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36	492	97.4	37921	2	AC008014 Homo sapi
37	492	97.4	37921	2	AC008014 Homo sapi
38	492	97.4	37921	2	AC008014 Homo sapi
39	492	97.4	37921	2	AC008014 Homo sapi
40	492	97.4	37921	2	AC008014 Homo sapi
41	492	97.4	37921	2	AC008014 Homo sapi

Pred. No. is the number of results predicted by chance to have a





























Search completed: January 4, 2003, 15:05:04  
Job time : 1952.47 secs

QY 430 GAGAAAGCTCTTGATTAAGATTAAGAAATCAAGGAGATTAAGAAATTAAGAAATTAAGAA 494  
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DB 185164 TGACATAGTAAGACCGGAGAGACTAGAGAGATATCTAGAGTTTTCAGAGATAAATATATATA 185105  
|||||  
QY 495 ATTTCAGAAATAGAAAGAAATGAAAGAAATTCATTAATAGAAATTAAGAAATTAAGAAATTAAGAA 454  
|||||  
DB 185104 ATGCTAATAATAGAAAGAAAGAAAGAGATTAATAGAGATTAAGAGATTAAGAGATTAAGAGATTA 185045  
|||||  
QY 455 AAAGTATTCAAGAGATTA 473  
|||||  
DB 185044 AATATTTCGCGGCTAATAA 185026  
|||||

## RESULT 15

AX281466/C

LOCUS

DEFINITION

SEQUENCE 40 from Patent WO0177476,

AX281466

VERSION

AX281466.1 GI:16608621

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 15674

Zinc-finger "synthetic construct"

Zinc-finger "synthetic construct"

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Zinc-finger "synthetic construct"

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 09:33:36, Search time 1296.06 seconds  
(without alignments)  
11249.881 Million cell updates/sec

Title: US-09-776-705-3\_COPY\_15000\_15500  
Perfect score: 501  
Sequence: 1 atgtggagattattatcat.....tgacaaagatgagagaaac 501

Scoring table: IUPAC1Y\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2051640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenBank:  
1: gb\_ba:  
2: gb\_hg:  
3: gb\_in:  
4: gb\_cm:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vt:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_ov:  
22: em\_pat:  
23: em\_ph:  
24: em\_pl:  
25: em\_ro:  
26: em\_sts:  
27: em\_un:  
28: em\_vt:  
29: em\_vt:  
30: em\_hg\_hum:  
31: em\_hg\_inv:  
32: em\_hg\_other:  
33: em\_hg\_mus:  
34: em\_hg\_pln:  
35: em\_hg\_rtd:  
36: em\_hg\_mam:  
37: em\_hg\_vrt:  
38: em\_sy:  
39: em\_hgo\_hum:  
40: em\_hgo\_mus:  
41: em\_hgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	IP	Description
C 1	501	100.0	37921	9	AC005854	AC005854 Homo sapi
C 2	420	67.8	167539	9	AC008914	AC008914 Homo sapi
C 3	400	97.8	244100	6	AC080136	AC080136 Homo sapi
C 4	52.6	10.5	11049	6	AX281156	AX281156 Sequence
C 5	52.6	10.5	11049	6	AX445570	AX445570 Sequence
C 6	52.6	10.5	11049	6	AX456394	AX456394 Sequence
C 7	52.4	10.5	86371	5	AC055672	AC055672 Homo sapi
C 8	51.4	10.3	178273	5	AC025621	AC025621 Homo sapi
C 9	51.6	10.3	191908	9	AC094803	AC094803 Homo sapi
C 10	50	10.0	10176	3	AF001370	AF001370 Homo sapi
C 11	50	10.0	145430	2	AL845421	AL845421 Homo sapi
C 12	50	10.0	261614	2	AL003653	AL003653 Homo sapi
C 13	49.4	9.9	2212	3	MIMTRNA	MIMTRNA
C 14	49.4	9.9	106434	3	AC117089	AC117089 Homo sapi
C 15	49.4	9.9	110990	2	U1M411.2	U1M411.2
C 16	49.2	9.8	25117	2	AC116102	AC116102 Homo sapi
C 17	49.2	9.8	192319	2	AL845339	AL845339 Homo sapi
C 18	49	9.8	112124	5	AL137184	AL137184 Homo sapi
C 19	48.4	9.7	44996	3	087145	087145 Homo sapi
C 20	48.4	9.7	162214	9	AC093809	AC093809 Homo sapi
C 21	48.4	9.7	195517	9	AL353741	AL353741 Homo sapi
C 22	49.2	9.6	6377	6	AX346138	AX346138 Sequence
C 23	49.2	9.6	172976	2	AC025821	AC025821 Homo sapi
C 24	48	9.6	118001	5	AC073081	AC073081 Homo sapi
C 25	47.4	9.5	157320	2	AC118889	AC118889 Homo sapi
C 26	47.4	9.5	188581	10	AL678004	AL678004 Homo sapi
C 27	47.2	9.1	5528	3	AC201421	AC201421 Homo sapi
C 28	47.2	9.1	3055	3	AX083745	AX083745 Sequence
C 29	46.6	9.1	143501	2	AC116936	AC116936 Homo sapi
C 30	46.2	9.2	5940	3	AC114259	AC114259 Homo sapi
C 31	46.2	9.2	145514	2	AC006872	AC006872 Homo sapi
C 32	46.2	9.2	54980	6	AX344564	AX344564 Sequence
C 33	46	9.2	77193	9	AL450347	AL450347 Homo sapi
C 34	46	9.2	42469	2	AC116340	AC116340 Homo sapi
C 35	46	9.2	176976	2	AC025842	AC025842 Homo sapi
C 36	45.8	9.1	14924	6	AX345127	AX345127 Sequence
C 37	45.8	9.1	14924	6	AX345127	AX345127 Sequence
C 38	45.8	9.1	129457	9	AC087507	AC087507 Homo sapi
C 39	45.8	9.1	168509	2	AC015570	AC015570 Homo sapi
C 40	45.8	9.1	171717	2	AC009266	AC009266 Homo sapi
C 41	45.8	9.1	181033	10	AL731663	AL731663 Homo sapi
C 42	45.8	9.1	185210	10	AL606410	AL606410 Homo sapi
C 43	45.8	9.1	190550	2	AP001797	AP001797 Homo sapi
C 44	45.6	9.1	8467	6	AX445010	AX445010 Sequence
C 45	45.6	9.1	11046	6	AX277955	AX277955 Sequence

# ALIGNMENTS

RESULT 1	AC005854/c	37921 bp	OMA	Human	BAR-1999
AC005854	Homo sapiens, complete sequence				
DEFINITION	AC005854				
ACCESSION	AC005854.2	GI:4454568			
KEYWORDS	HLG				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 37921)				
AUTHORS	Montgomery K.T., Lau S.L. and Kucherlapati R.				
TITLE	High Throughput Sequencing of Human Chromosome 12				
JOURNAL	unpublished				















[illegible]

NOTE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

this sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an appropriate chemistry, or covered by high quality data (i.e., phred quality  $\geq 30$ ): an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

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repeat_region 14317..14429 /rpt_family="L1"
repeat_region 14424..14446 /rpt_family="AT_rich"
repeat_region 14761..14780 /rpt_family="L1"
repeat_region 15858..16070 /rpt_family="(AAAA)n"
repeat_region 16092..16121 /rpt_family="L2"
repeat_region 16132..16413 /rpt_family="(TTTA)n"
repeat_region 17001..17265 /rpt_family="Alu"
repeat_region 18228..18954 /rpt_family="MaLR"
repeat_region 19376..19524 /rpt_family="MIR"
repeat_region 19688..20131 /rpt_family="MaLR"
repeat_region 21251..21272 /rpt_family="ERV1"
repeat_region 21519..21745 /rpt_family="(TG)n"
repeat_region 21737..21759 /rpt_family="Alu"
repeat_region 22840..22772 /rpt_family="AT_rich"
repeat_region 23379..23493 /rpt_family="MaLR"
repeat_region 23475..23509 /rpt_family="MIR"
repeat_region 24800..24825 /rpt_family="AT_rich"
repeat_region 25222..25267 /rpt_family="L1"
repeat_region 25340..25453 /rpt_family="(TAAAA)n"
repeat_region 25591..25659 /rpt_family="MaLR"
repeat_region 26216..26957 /rpt_family="AT_rich"
repeat_region 27143..27898 /rpt_family="L2"
repeat_region 28048..28103 /rpt_family="L2"
repeat_region 28111..28219 /rpt_family="L1"
repeat_region 28279..28321 /rpt_family="L1"
repeat_region 28548..28944 /rpt_family="AT_rich"
repeat_region 28571..28601 /rpt_family="MaLR"
repeat_region 30995..31015 /rpt_family="AT_rich"
repeat_region 31230..31590 /rpt_family="(TA)n"
repeat_region 32955..33236 /rpt_family="MaLR"
repeat_region 33235..33305 /rpt_family="MaLR"
repeat_region 33235..33305 /rpt_family="(TTTAA)n"

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Query Match: 10.3%; Score 51.6; DB 9; Length 178378;  
Best Local Similarity 51.8%; Pred. No. 0.51;  
Matches 117; Conservative 0; Mismatches 109, Indels 0; Gaps 0;

95 TTAAGTGGCGTTAGCAAAATTCACCTAAGGATGTAGACACACTTAAGATTTCAT 154  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
bb 117717 TA AACAGGCTTTTAGAAAAAAAATTTTAAGCTCTTCTGCACAAATTGAATTTGAT 117776  
  
155 GTAAAAATTGGAGTGCTATTTTTAACAGCAATCTTTGCCCATGGTGTCACAAATAACG 214























Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,  
 Lozano, K., Lu, X., Lucier, R., Lucia, R., Luna, R., Ma, J.,  
 Maheshwari, S., Mapua, F., Martin, R., Martindale, A., Martinez, E.,  
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 Nguyen, N., Nikooset, P., Niekirk, S., Ogata, M., Okumura, G.,  
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 Peters, L., Piatys, P., Piatys, R., Pu, B. L., Quiles, M., Ken, Y.,  
 Rivers, M., Rojas, A., Rojebokan, J., Rolfe, M., Ruiz, S., Savary, G.,  
 Scher, S., Scott, G., Shen, H., Shoshitani, N., Sisson, I.,  
 Sodergren, E., Sonak, P., Sparks, A., Stanley, H., Stone, H.,  
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 Tanczyk, J., Taylor, C., Taylor, V., Teitob, D., Thomas, N., Thomas, S.,  
 Usmani, K., Vasquez, L., Vega, V., Villalobos, D., Vinson, R., Wang, Q.,  
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,  
 Williams, G., Williamson, A., Wierzyk, E., Woodson, S., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,  
 Weinstein, G., and Gibbs, R.

# TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

1. (bases 1 to 244100)  
 2. (bases 1 to 244100)  
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## PEPERENCE TITLE JOURNAL

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Gabisi, A., Guo, J., Garcia, A., Garner, J., Gatch, N., Gill, R.,  
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 Tansey, J., Taylor, J., Taylor, J., Taylor, J., Taylor, J., Taylor, J.,  
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 Williams, G., Williamson, A., Wolczyk, B., Wood, S., Wolley, K.,  
 Wu, C., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y.,  
 Wolstock, G., and others.  
 Direct Submission  
 Unpublished  
 (bases 1 to 13740)  
 Worley, K.C.  
 Direct Submission  
 Submitted (07-DEG-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 (bases 1 to 13740)  
 Worley, K.C.  
 Direct Submission  
 Submitted (12-01-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 on Jul 11, 2002 this sequence version replaced at:18846163.  
 -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgs.bcm.tmc.edu/>  
 Contact: [base-help@bcm.tmc.edu](mailto:base-help@bcm.tmc.edu)  
 -----  
 Project Information  
 Center project name: G1Q0  
 Center clone name: CH230.13467  
 -----  
 Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.96b20  
 Consensus quality: 84753 bases at least Q40  
 Consensus quality: 89822 bases at least Q40  
 Consensus quality: 94620 bases at least Q20  
 -----  
 \* Note: Estimated insert size may differ from sequence length  
 \* <http://www.ncbi.nlm.nih.gov/Genbank/seq/seq.html>  
 \* Note: This is a "working draft" sequence. It currently  
 \* consists of 60 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of Ns, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence,  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1154: contig of 1154 bp in length  
 \* 1155 1254: gap of unknown length  
 \* 1255 2403: contig of 1149 bp in length  
 \* 2404 2504: gap of unknown length  
 \* 2504 4658: contig of 1155 bp in length



```

Falls, L., Ferrante, D., Flann, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Girrell, J., Guevara, W., Guiraud, P., Hahn, S., Hamilton, K.,
Harris, C., Harris, E., Har, H., Hrdlick, P., Hryciw, A., Hrynchuk, J.,
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Jachson, R., G. Y., Johnson, W., Joliet, S., Joudah, S.,
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Li, J., Li, Z., Liechman, A., Liu, C., Liu, J., Liu, W., Louis, B.,
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Sutton, A., Sutton, A., Sutton, A., Sutton, A., Sutton, A., Sutton, A.,
Tasey, J., Taylor, A., Taylor, A., Taylor, A., Taylor, A., Taylor, A.,
Tasman, K., Vasquez, L., Vega, V., Villalobos, P., Viscusi, R., Wang, S.,
Wang, S., Ward-Moore, S., Warren, P., Washington, C., Washington, S.,
Williams, G., Williams, A., Williams, A., Williams, A., Williams, A.,
Wu, C., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y., Wu, Y.,
Weinstock, G., and Gibbs, R.

Direct Submission
2 (bases 1 to 184007)
Worley, K.C.
Submitted (01-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
1 (bases 1 to 184007)
Worley, K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
on Jul 18, 2002 this sequence version replaced at:20514476.
-----
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgc-help@bcm.tmc.edu
-----
Project Information
Center project name: GW03
Center clone name: CH230_2862
-----
Summary Statistics
Sequencing vector: plasmid
Chemistry: Dye-terminator Run type: 100% of reads
Assembly program: Phrap; version 0.99029
Consensus quality: 14050 bases at least Q40
Consensus quality: 14935 bases at least Q30
Consensus quality: 142357 bases at least Q20
-----
* Note: Estimated insert size may differ from sequence length
* for CH230_2862. For example, 144,300 bp in length.
* NOTE: This is a working draft sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence,
* as soon as it is available and the accession number will
* be preserved.
* 1 1057: contig of 1057 bp in length
* 1058 2490: gap of unknown length
* 1158 2490: contig of 1224 bp in length
* 2481 2480: gap of unknown length

```











1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems.

2. The second section focuses on the role of technology in modern record management. It highlights how cloud storage and data analytics tools can enhance the efficiency and security of record-keeping processes. The author provides examples of software solutions and discusses the benefits of automation in reducing human error and improving data accessibility.

3. The third part of the document addresses the legal and regulatory requirements for record-keeping. It reviews relevant laws and standards, such as the General Data Protection Regulation (GDPR) and industry-specific compliance frameworks. The text offers practical advice on how to ensure that record-keeping practices align with these legal obligations.

4. The fourth section explores the challenges associated with long-term data preservation. It discusses the risks of data degradation, loss, and unauthorized access over time. The author suggests strategies for mitigating these risks, such as regular backups, disaster recovery plans, and secure storage environments.

5. The final part of the document provides a summary of key findings and recommendations. It reiterates the importance of a proactive approach to record management and encourages the adoption of best practices. The text concludes with a call to action, urging organizations to regularly review and update their record-keeping policies to stay current with evolving technologies and regulations.





CC process e.d. cellular proliferation, growth, differentiation, or  
 CC migration, which is useful in treatment and diagnosis of transport  
 CC associated disorders. These disorders include central nervous system  
 CC (CNS) disorders, autoimmune function disorders, learning or memory  
 CC disorders, bipolar affective neurological disorders, cardiac-related  
 CC disorders, cancer, tumour angiogenesis and metastasis, skeletal  
 CC dysplasia, hepatic disorders, haematopoietic and/or myelopoietic  
 CC disorder, hormonal disorders, and immune disorders. The polypeptides and  
 CC polypeptides, and homologues of the polynucleotides and antibodies,  
 CC are useful for screening assays, predictive medicine (e.g. diagnostic  
 CC assays, prognostic assays, monitoring clinical trials, and  
 CC pharmacogenetics) and treatment (e.g. therapeutic and prophylactic).

XX Sequence 4767 BP: 1157 A: 713 C: 690 G: 1267 T: 0 others:

Query Map: 99.79; Score 496.4; PB 24; Length 7767;

Best Local Similarity 99.8%; Pred. No. 4.2e-100;

Matches 500; Overlapping 0; Mismatches 1; Labels 0; Gaps 0;

```

QY 1 AATAGATTTTGTAAATGTTAAACATCTATATTTAAAGTTAAACACTAAATATAGAG 60
   |||||||
DB 2427 AATAGATTTTGTAAAGTTAAACATCTATATTTAAAGTTAAACACTAAATATAGAG 2486
   |||||||
QY 61 AGGAGCTTTTATTCATCATAGCAACACACAAATTAAGTGTATAGCTAAATAGCTG 120
   |||||||
DB 2487 AGGAGCTTTTATTCATCATAGCAACACACAAATTAAGTGTATAGCTAAATAGCTG 2546
   |||||||
QY 121 TTCTAAGAGCAICGCTTTTCATGTTATTCGTAATGCTGCTGCTATACCTTTGTCAT 180
   |||||||
DB 2547 TTCTAAGAGCAICGCTTTTCATGTTATTCGTAATGCTGCTGCTATACCTTTGTCAT 2606
   |||||||
QY 181 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
   |||||||
DB 2607 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2666
   |||||||
QY 241 GTGAGATACACATACAGAGATTTTGTGATATTTTGTGATATTTTGTGATATTTTGT 2796
   |||||||
DB 2667 GTGAGATACACATACAGAGATTTTGTGATATTTTGTGATATTTTGTGATATTTTGT 2856
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QY 301 GAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
   |||||||
DB 2727 GAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2796
   |||||||
QY 361 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 420
   |||||||
DB 2797 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2846
   |||||||
QY 421 AGCATTTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
   |||||||
DB 2847 AGCATTTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2906
   |||||||
QY 481 CATATTTATCTCTGATCAAAAT 501
   |||||||
DB 2907 CATATTTATCTCTGATCAAAAT 2927
   |||||||

```

## RESULT 3

AAL21895

ID AAL21895 standard; cDNA, 472 BP.

XX AC

XX AAL21895;

XX 07-DEC-2001 (first entry)

XX Human breast cancer expressed polynucleotide 1452.

XX Human breast cancer; cell marker; cytostatic; ss.

XX Homo sapiens.

XX W260151628-A2.

XX 07-JUL-2001.

XX 19-DEC-2001 (first entry)

XX 10-JAN-2001; 2001W: US000798.

XX 14-JAN-2001; 2001S: 0176077.

XX 14-MAR-2001; 2001S: 0189177.

XX 24-MAR-2001; 2000S: 0192099.

XX 25-MAR-2001; 2001S: 0193430.

XX 15-MAY-2000; 2000S: 0205240.

XX 09-JUN-2000; 2000S: 0211315.

XX 25-JUL-2000; 2000S: 0220544.

XX (MILLER) MILLERINDB PREDICTIVE MUTATION INC.

XX Little L, Xu Y, Wang Y, Steinhardt K;

XX WEL, 2001 47676748.

XX New peptide useful as a marker for the diagnosis of breast cancer

XX Claim 1; page 2572; 3695pp; English.

XX the invention relates to human breast cancer expressed polynucleotides  
 XX (AAL07544-AAL26799) and methods of assessing whether a patient is  
 XX afflicted with breast cancer by examining the correlation between the  
 XX expression of certain markers and the various state of breast cells.  
 XX The polynucleotides 1452 and encoded polypeptides are potential markers for  
 XX detecting, diagnosing, monitoring, characterising treatment and  
 XX potentially preventing breast cancer. The polynucleotides and encoded  
 XX polypeptides are also useful for isolating compounds with cytostatic  
 XX activity.

XX Sequence 472 BP: 150 A: 86 C: 690 G: 1267 T: 0 others:

Query Map: 79.29; Score 37.4; PB 22; Length 472;  
 Best Local Similarity 99.7%; Pred. No. 5.2e-72;  
 Matches 411; Overlapping 0; Mismatches 1; Labels 0; Gaps 0;

QY 1 AATAAGATTTTGTAAATGTTAAACATCTATATTTAAAGTTAAACACTAAATATAGAG 60

DB 100 AATAAGATTTTGTAAATGTTAAACATCTATATTTAAAGTTAAACACTAAATATAGAG 159

QY 61 AGGAGCTTTTATTCATCATAGCAACACACAAATTAAGTGTATAGCTAAATAGCTG 120

DB 160 AGGAGCTTTTATTCATCATAGCAACACACAAATTAAGTGTATAGCTAAATAGCTG 219

QY 121 TTCTAAGAGCAICGCTTTTCATGTTATTCGTAATGCTGCTGCTATACCTTTGTCAT 180

DB 223 TTCTAAGAGCAICGCTTTTCATGTTATTCGTAATGCTGCTGCTATACCTTTGTCAT 274

QY 181 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

DB 280 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 339

QY 241 GTGAGATACACATACAGAGATTTTGTGATATTTTGTGATATTTTGTGATATTTTGT 300

DB 340 GTGAGATACACATACAGAGATTTTGTGATATTTTGTGATATTTTGTGATATTTTGT 399

QY 361 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 420

DB 400 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 459

QY 461 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 469

DB 460 AATGTAAGTACATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 469

RESULT 4

AAL13025

II AAL13025 standard; cDNA, 466 BP.

XX X

XX AAL13025;

XX 07-DEC-2001 (first entry)





Query Match: 24.6%, Score 118; DB 21; Length 455;  
 Best Local Similarity: 100.0%; Pred. No. 86-17;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATAGATTTCGTAAGGTTAAAGATATATATTAAGTTTAAAGATATAGAG 63  
 UUU  
 DB 237 AATAGATTTCGTAAGGTTAAAGATATATATTAAGTTTAAAGATATAGAG 236  
 UUU  
 QY 63 AATAGATTTCGTAAGGTTAAAGATATATATTAAGTTTAAAGATATAG 118  
 UUU  
 DB 297 AATAGATTTCGTAAGGTTAAAGATATATATTAAGTTTAAAGATATAG 296  
 UUU

RESULT 8  
 AAS45489  
 ID AAS45489 standard, DNA, 15732 BP.  
 XX  
 AC AAS45489;  
 DE 18-DEC-2004 (first entry)  
 XX  
 DE Chemically pretreated complementary DNA associated with cell cycle #47.  
 XX  
 KW cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging;  
 KW human immunodeficiency virus; neurodegenerative disorder; solid tumor;  
 KW arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;  
 KW tumor suppressor; anti-tumor; cytosine; anti-tumor; cancer; HIV;  
 KW PCR primer.  
 XX  
 SS Homo sapiens.  
 XX  
 PR W203168911 A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 FE 15-MAR-2001; 2001W0-EP02945.  
 XX  
 PR 15-MAR-2001; 2000DE-1019058.  
 PR 06-APR-2000; 2000DE-1019174.  
 PR 07-APR-2000; 2000DE-1019174.  
 PR 30-JUN-2000; 2000DE-1042529.  
 PR 01-SEP-2000; 2000DE-1042529.  
 XX  
 PA (EPIC-) EPIDEMIOLOGY AG.  
 XX  
 PI olek A. Piepenbrock C., Berlin K;  
 DE WPI; 2001-602751/68.  
 XX  
 PI sequencing primers and probes for analysing diseases associated with  
 PI cytosine methylation state e.g. arthritis, cancer, aging,  
 PI arteriosclerosis comprising fragments of chemically modified genes  
 PI associated with cell cycle  
 XX  
 PI Claim 1; SEQ ID No 94; 28pp; English.

Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA  
 molecules associated with the cell cycle and specific PCR primers of the  
 invention. The sequences are useful for detecting the methylation state  
 of all CpG dinucleotides in a sequence and therefore for analysing  
 associated diseases. By analysing cytosine methylation in the pretreated  
 DNA, genetic and/or epigenetic parameters for the diagnosis and therapy  
 of existing diseases or the predisposition to specific diseases can be  
 ascertained. The parameters may be compared to another set of genetic  
 and/or epigenetic parameters, the differences serving as basis for  
 diagnosis and/or prognosis events which are disadvantageous to patients.  
 The sequences of the invention are useful for the diagnosis and therapy  
 of HIV infection, neurodegenerative disorders, arthritis, cancer, heart  
 aging, glomerular disease, low body disease, arthritis,  
 arteriosclerosis, solid tumors and cancers.

80 Sequence 15742 BP; 5557 A; 70 C; 2865 G; 7249 T; 0 other;  
 Query Match: 11.0%; Score 55; DB 22; Length 15742;  
 Best Local Similarity: 51.4%; Pred. No. 0.008;  
 Matches 127; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 218 ACAAATTTTAAAGACACACATCTGCGAGATACACTACACAGATTTGTTGATACATTTT 277  
 UUU  
 DB 5904 AAGAGTATATAGAAAATTTTAAATTTTAAATATATTTTATGTAAGTGAAGATTTT 5964  
 UUU  
 QY 278 TATTTGATATAACATCTGAGTCAGCAAACTGCTATATGTTTATGATATATAATCT 347  
 UUU  
 DB 5964 TTTTATATAAATCTTACGCAATAATATATATAGTACATGTTAAATTTATTTAIGATAT 6024  
 UUU  
 QY 348 TATTTCTATATCATCAGAAATTTAATGATAGTACATTTTATTTTATTTTACATG 407  
 UUU  
 DB 6024 GATTAATTAAGGTTTATTTTGAATGATGATGTTTATTTATTAAGTAATAATTTAAT 6084  
 UUU  
 QY 498 TATTTTCTTCTTCACAGTCAAAACATTTATATTAATGCGGCTGAGGAGAGATATAA 457  
 UUU  
 DB 6084 ATTTTAAAGGTAAGATATGAAATATTTTTTTTTTTTTTTTAAAGATGAGGAAATAT 6144  
 UUU  
 QY 458 GTTGGTG 464  
 UUU  
 DB 6144 ATATATG 6150

RESULT 9  
 ABE25234  
 ID ABE25234 standard, DNA, 15742 BP.  
 XX  
 AC ABE25234;  
 DE 23-APR-2002 (first entry)  
 XX  
 DE DNA transcription associated complementary genomic DNA #59.  
 XX  
 KW DNA; cytosine methylation state; CpG; retroviral infection; gene; de;  
 KW single nucleotide polymorphism; adenosine deaminase deficiency; cancer;  
 KW viral infection; seizure syndrome; hematological disorder; tuberculosis;  
 KW immunological disorder; Werner syndrome; developmental disorder;  
 KW psoriasis; Koster's syndrome; neurological disorder; erythropoiesis;  
 KW neurodegenerative disorder; Waardenburg syndrome; glomerular disease;  
 KW myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;  
 KW arteriosclerosis; congenital heart disease; HIV syndrome; gene therapy;  
 KW polytumor disorder; solid tumor.  
 XX  
 SS Unidentified.  
 XX  
 PR W200192565-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 FE 06-APR-2001; 2001W0-EP04974.  
 XX  
 PR 06-APR-2000; 2000DE-1019058.  
 PR 07-APR-2000; 2000DE-1019174.  
 PR 30-JUN-2000; 2000DE-1042529.  
 PR 01-SEP-2000; 2000DE-1042529.  
 XX  
 PA (EPIC-) EPIDEMIOLOGY AG.  
 XX  
 PI olek A. Piepenbrock C., Berlin K;  
 DE WPI; 2002-090346/12.  
 XX  
 PI New nucleic acids or oligomers, useful for diagnosing or treating  
 PI diseases associated with DNA transcription, e.g. immunological  
 PI disorders, Werner syndrome, psoriasis, myocardial infarction, solid  
 PI tumours or cancer  
 XX  
 PI Claim 1; SEQ ID No 108; 42pp; English.







## RESULTS

ABL4157  
ID ABL4157 standard: INA; 16766 BP.

XX

XX A:

XX ABL4157:

XX 26 MAR-2002 (first entry)

XX

XX Human immune system associated gene SEQ ID NO: 2130.

XX

XX Human: immune system disease; cytosine methylation; antiasthmatic;

XX

XX anti-fatherless; anti-leukemia; cytosine; neotrophic;

XX

XX neoprotective; anti-HIV; anticonvulsant; ophthalmologic;

XX

XX anti-inflammatory; anti-arthritic; antidiabetic; antipsoriatic;

XX

XX anti-inflammatory; cancer; eye disease; arteriosclerosis; anemia;

XX

XX acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;

XX

XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

XX

XX gene; ds.

XX

XX Homo sapiens.

XX

XX W200200928-A2.

XX

XX 18-JAN-2002.

XX

XX 02-JUL-2001; 2001W-EP07547.

XX

XX 30-JUN-2000; 2000DE-1042529.

XX

XX 01-SEP-2000; 2000DE-1043826.

XX

XX (EPIC-) EPIGENOMICS AG.

XX

XX Alex A. Piepenbrock C, Berlin K;

XX

XX WP1; 2002-130009/17.

XX

XX Nucleic acid comprising treatment of chemically modified gene, used

XX

XX for diagnosis and treatment of diseases associated with abnormal

XX

XX cytosine methylation.

XX

XX Claim 1: SEQ ID NO 2130; 32pp - Sequence listing: German.

XX

XX the present invention provides a number of human immune system associated

XX

XX genes which are modified by the methylation of cytosines. The sequences

XX

XX can be used in the diagnosis and treatment of immune system disorders,

XX

XX including eye diseases such as retinopathy, neovascular glaucoma and

XX

XX macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid

XX

XX leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

XX

XX rheumatoid arthritis, psoriasis and inflammatory/digestive bowel

XX

XX diseases. The present sequence is a gene of the invention.

XX

XX Sequences 16766 BP; 4604 A; 267 C; 4632 G; 8263 T; 0 other;

XX

XX Query Match 9.7%; Score 48.6; DB 24; Length 16766;

XX

XX Best Local Similarity 52.7%; Pred. No. 0.2;

XX

XX Matches 128; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 497 GAA 499

DB 11

DB 1529 GAA 1531

Search completed: January 4, 2003, 15:10:19

Job time : 142.726 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 09:40:56 : Search time 752.955 Seconds  
(without alignments)  
10634.887 Million cell updates/sec

Title: us-09-776-705-3\_copy\_30000\_30500

Perfect score: 501  
Sequence: 1 autaatatttgaataatt  
alignatatttgaataatt 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 1249912

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estlin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_estic.\*  
9: qb\_estll.\*  
10: qb\_estl2.\*  
11: qb\_estc.\*  
12: qb\_est3.\*  
13: qb\_est4.\*  
14: qb\_est5.\*  
15: em\_estlum.\*  
16: em\_estom.\*  
17: qb\_estt.\*  
18: em\_estss\_hum.\*  
19: em\_estss\_fov.\*  
20: em\_estss\_pln.\*  
21: em\_estss\_vit.\*  
22: em\_estss\_fun.\*  
23: em\_estss\_mum.\*  
24: em\_estss\_sus.\*  
25: em\_estss\_other.\*  
26: em\_estss\_pro.\*  
27: em\_estss\_rod.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	501	100.0	749	12	BC568069
2	178	95.4	656	12	BC565874
3	405	80.8	405	10	AV653985
4	259.2	51.7	454	10	AV660303
5	211.8	42.3	287	16	AV653997
6	203.4	40.6	515	14	B0031502

7	201.8	40.3	534	9	AI146007
8	200.8	41.1	1501	11	AK006626
9	195.8	45.1	510	9	AI15747
10	185	46.9	458	9	AI146986
11	194	40.7	729	12	BC548592
12	145	29.7	487	10	AV648042
13	149	29.7	487	10	AV648278
14	149	29.7	496	10	AV649219
15	149	29.7	406	10	AV648431
16	145	29.7	609	13	AV648144
17	149	29.7	695	10	AV648554
18	145	29.7	792	10	AV649505
19	146	29.1	754	12	BC543466
20	111	27.1	411	9	AA250197
21	134	29.7	734	12	BC290658
22	109	21.8	474	14	B00862
23	109	21.8	475	14	B05836
24	78.2	15.6	469	9	AA540730
25	62	12.4	463	17	CNS00441
26	60.4	12.1	987	17	CNS01493
27	57	11.0	524	17	CNS00120
28	58.8	11.7	931	19	CNS00120
29	57.2	11.4	862	17	BH152813
30	56.8	11.3	1101	17	CNS00393
31	56.6	11.3	876	17	CNS009XJ
32	56.4	11.3	996	12	CNS004FH
33	56.2	11.2	923	17	CNS006K3
34	56.8	11.1	459	13	BH152578
35	55.8	11.1	1101	17	CNS000EV
36	54.8	11.0	1101	17	CNS00112
37	54	11.0	1169	17	CNS006H1
38	54.4	10.5	878	17	CNS01878
39	52	10.4	1204	17	CNS016E2
40	51.4	10.3	1084	17	CNS006H3
41	51.4	10.3	1091	17	CNS0074F
42	51.4	10.3	1125	9	AI1547603
43	51.2	10.2	818	14	BQ144786
44	50.8	10.1	1101	17	CNS00384
45	50.6	10.1	797	9	AI1556423

## ALIGNMENTS

EST: 1	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
LOCUS	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
DEFINITION	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
ACCESSION	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
VERSION	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
KEYWORDS	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
SOURCE	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
ORGANISM	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
REFERENCE	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
AUTHORS	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
TITLE	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
JOURNAL	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001
COMMENT	RG568069	749 bp	mRNA	Linear	EST 10 APR 2001

source:















```

source
1. 387
Zordanism: "Homo sapiens"
ZB_xref: "axoni:9606"
Zclone_lib: "GLC"
Zissue_type: "corresponding non-carcinoma liver tissue"
Zstage: "Adult"
Zlab_host: "Solk"
Zseq: "Wistar-Kyoto"
Xhol:
BASE COUNT 113 a 49 c 72 g 15 t
ORIGIN

Query Match
Best Local Similarity 29.7% Score 149; DB 10; Length 387;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 412
DB 1 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 60
QY 413 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 472
DB 61 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 120
QY 473 ATCTCATTCATGTATCTGTCGTACAAAT 501
DB 121 ATCTCATTCATGTATCTGTCGTACAAAT 149

RESULT 14
AV648215
LOCUS AV648215 GLC Homo sapiens cDNA clone GLCRA09.3; mRNA sequence.
DEFINITION AV648215
ACCESSION AV648215.1 GI:9869229
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 496)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, S., Cai, L., Zhang, X.,
Xiao, H., Guo, J., Liu, F., Huang, Q., Cheng, Z., Lin, Z., Du, J., Hu, W.,
Shen, Y., Fu, S., Fan, Z., Zheng, W., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncarcinous liver
[Proc. Natl. Acad. Sci. U.S.A. 98 (24): 15085-15094 (2001)]
21625106
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhaqjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801922 (ex.45)
Fax: 86-21-50801922
Email: hanzq@chao.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 396
Zordanism: "Homo sapiens"
ZB_xref: "axoni:9606"
Zclone_lib: "GLC"
Zissue_type: "corresponding non-carcinoma liver tissue"
Zstage: "Adult"
Zlab_host: "Solk"
Zseq: "Wistar-Kyoto"
Xhol:
BASE COUNT 117 a 51 c 72 g 15 t
ORIGIN

```

```

Query Match
Best Local Similarity 29.7% Score 149; DB 10; Length 387;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 412
DB 1 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 60
QY 413 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 472
DB 61 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 120
QY 473 ATCTCATTCATGTATCTGTCGTACAAAT 501
DB 121 ATCTCATTCATGTATCTGTCGTACAAAT 149

RESULT 15
AV648341
LOCUS AV648341 GLC Homo sapiens cDNA clone GLCRA09.3; mRNA sequence.
DEFINITION AV648341
ACCESSION AV648341
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 496)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, S., Cai, L., Zhang, X.,
Xiao, H., Guo, J., Liu, F., Huang, Q., Cheng, Z., Lin, Z., Du, J., Hu, W.,
Shen, Y., Fu, S., Fan, Z., Zheng, W., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncarcinous liver
[Proc. Natl. Acad. Sci. U.S.A. 98 (24): 15085-15094 (2001)]
21625106
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhaqjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801922 (ex.45)
Fax: 86-21-50801922
Email: hanzq@chao.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 406
Zordanism: "Homo sapiens"
ZB_xref: "axoni:9606"
Zclone_lib: "GLC"
Zissue_type: "corresponding non-carcinoma liver tissue"
Zstage: "Adult"
Zlab_host: "Solk"
Zseq: "Wistar-Kyoto"
Xhol:
BASE COUNT 122 a 53 c 72 g 15 t
ORIGIN

Query Match
Best Local Similarity 29.7% Score 149; DB 10; Length 406;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 412
DB 1 AGAAGTTAATGAGTACATTCATTTTATTTTACAGTGTAGTCTTCTTCTTC 60
QY 413 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 472
DB 61 ACAGCAAAAGCAATTAATTTATTTGGGTCGAGGCAAGTAAAGTGTGGTGGAA 120
QY 473 ATCTCATTCATGTATCTGTCGTACAAAT 501

```























## RESULTS 14

010151010

# LIST

DEFINITION

## APPENDIX

ACQUISITION  
VERSION

KEYWORDS

## NOTES

ORGANIZER

UNIVERSITY



GenCore version 5.1.3  
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CM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 11:06:05 : Search time 103.597 Seconds

(without alignments)

7606.585 Million cell updates/sec

Title: us-09-776-705-1

Perfected score: 1822

Sequence: 1 ccattccaaacatcagga.....cattagacaaagaaataac 1922

Scoring table: IDENTITY\_NUC

Gapop 10 0 0 Gapop 1 0

Searched: 481593 seqs 216250104 residues

Total number of hits satisfying chosen parameters: 76186

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: 1822 100.0 1822 10 US-09-776-705-1  
2: 1793.5 98.4 3769 10 US-09-960-232A-4  
3: 1637.6 89.9 1644 10 US-09-860-232A-6  
4: 1192.6 65.5 2313 10 US-09-789-919-16  
5: 1192.6 65.5 3857 10 US-09-789-919-65  
6: 555.4 40.5 776 10 US-09-741-972-214  
7: 420.8 24.1 4855 9 US-10-071-766-127  
8: 327.4 19.0 2431 10 US-09-919-497-17  
9: 327.4 18.0 2431 10 US-09-880-107-4372  
10: 277 15.2 292 10 US-09-564-761-20420  
11: 277 15.2 3273 10 US-09-776-705-3  
12: 210 11.5 478 10 US-09-864-761-12954  
13: 145.4 7.7 234 10 US-09-983-965-5090  
14: 127.5 7.0 333 10 US-09-867-701-1622  
15: 89.4 4.9 312 10 US-09-960-352-14353  
16: 57.8 3.2 143 10 US-09-958-598-1476  
17: 40.6 2.2 2116 10 US-09-508-711-167  
18: 38.2 2.1 1765 9 US-09-938-842A-1334  
19: 37.4 2.1 548 10 US-09-864-761-14757

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1822	100.0	1822	10 US-09-776-705-1	Sequence 1, Appli
2	1793.5	98.4	3769	10 US-09-960-232A-4	Sequence 4, Appli
3	1637.6	89.9	1644	10 US-09-860-232A-6	Sequence 6, Appli
4	1192.6	65.5	2313	10 US-09-789-919-16	Sequence 19, Appli
5	1192.6	65.5	3857	10 US-09-789-919-65	Sequence 65, Appli
6	555.4	40.5	776	10 US-09-741-972-214	Sequence 214, Appli
7	420.8	24.1	4855	9 US-10-071-766-127	Sequence 127, Appli
8	327.4	19.0	2431	10 US-09-919-497-17	Sequence 17, Appli
9	327.4	18.0	2431	10 US-09-880-107-4372	Sequence 30420, A
10	277	15.2	292	10 US-09-564-761-20420	Sequence 3, Appli
11	277	15.2	3273	10 US-09-776-705-3	Sequence 3, Appli
12	210	11.5	478	10 US-09-864-761-12954	Sequence 5090, Ap
13	145.4	7.7	234	10 US-09-983-965-5090	Sequence 1726, Ap
14	127.5	7.0	333	10 US-09-867-701-1622	Sequence 14853, A
15	89.4	4.9	312	10 US-09-960-352-14353	Sequence 1476, Ap
16	57.8	3.2	143	10 US-09-958-598-1476	Sequence 167, Appl
17	40.6	2.2	2116	10 US-09-508-711-167	Sequence 1324, M
18	38.2	2.1	1765	9 US-09-938-842A-1334	Sequence 14757, A
19	37.4	2.1	548	10 US-09-864-761-14757	

C 20	36.8	2.0	2000	9 US-09-938-842A-1219	Sequence 1219, Ap
C 21	36.4	2.0	17669	9 US-09-736-457-1804	Sequence 1804, Ap
C 22	36.4	2.0	17669	9 US-09-932-941-1804	Sequence 1804, Ap
C 23	36.4	2.0	17669	9 US-09-849-626-1804	Sequence 1804, Ap
C 24	36	2.0	1872	10 US-09-815-242-4836	Sequence 4836, Ap
C 25	36	2.0	1884	10 US-09-815-242-6267	Sequence 6267, Ap
C 26	35.8	2.0	804	9 US-09-820-473-1	Sequence 1, Appli
C 27	35.8	2.0	804	10 US-09-820-408-1	Sequence 1, Appli
C 28	35.2	1.9	57459	10 US-09-864-472-4	Sequence 5, Appli
C 29	34.8	1.9	774	10 US-09-974-300-934	Sequence 934, Ap
C 30	34.8	1.9	4240	10 US-09-842-552-89	Sequence 89, Appli
C 31	34.6	1.9	588	10 US-09-864-761-14662	Sequence 14662, A
C 32	34.5	1.9	1535	9 US-09-736-626-2573	Sequence 2573, Ap
C 33	34.3	1.9	2130	10 US-09-879-652-7	Sequence 6, Appli
C 34	34.6	1.9	5728	10 US-09-617-800A-479	Sequence 479, Ap
C 35	34.4	1.9	6895	10 US-09-822-860A-341	Sequence 341, Ap
C 36	34.4	1.9	4147	10 US-09-925-301-158	Sequence 158, Ap
C 37	34.4	1.9	16744	10 US-09-902-466-281	Sequence 281, Ap
C 38	34.4	1.9	16744	10 US-09-904-824A-273	Sequence 273, Ap
C 39	34.2	1.9	2317	10 US-09-731-179-3	Sequence 3, Appli
C 40	34.2	1.9	2782	10 US-09-925-301-500	Sequence 500, Ap
C 41	34.3	1.9	3338	10 US-09-954-456-1933	Sequence 1933, Ap
C 42	34	1.9	495	9 US-09-894-841-41	Sequence 41, Appli
C 43	34	1.9	1593	9 US-09-938-842A-1859	Sequence 1859, Ap
C 44	34	1.9	2062	10 US-09-846-900A-2	Sequence 2, Appli
C 45	33.3	1.9	4525	10 US-09-961-940-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
us-09-776-705-1  
Sequence 1, Appli: 1822 100.0 1822 10 US-09-776-705  
Query: 1 ccattccaaacatcagga.....cattagacaaagaaataac 1922  
Target: 1 ccattccaaacatcagga.....cattagacaaagaaataac 1922  
Alignment: 1 ccattccaaacatcagga.....cattagacaaagaaataac 1922  
Score: 1822 100.0 1822 10 US-09-776-705  
Software: FASTSEQ for Windows Version 4.0  
Seq ID No: 1  
Length: 1822  
Type: DNA  
Organism: Human  
us-09-776-705-1

Query Match	100.0%	Score 1822	DB ID	Length 1822
Best Local Similarity	100.0%	Fixed No: 0		
Matches 1822	Conserved 100	Mismatches 0	Indels 0	Gaps 0
1	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
2	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
3	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
4	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
5	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
6	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
7	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
8	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
9	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
10	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
11	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
12	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
13	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
14	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
15	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
16	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
17	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
18	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
19	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
20	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
21	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
22	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
23	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
24	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
25	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
26	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
27	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
28	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
29	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
30	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
31	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
32	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
33	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
34	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
35	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
36	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
37	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
38	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
39	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
40	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
41	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
42	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
43	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
44	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1
45	ccattccaaacatcagga.....cattagacaaagaaataac 1922	100.0%	1822	10 US-09-776-705-1















Query March 18.0% Score 327.4; Db 10. Length 2431;  
Best Local Similarity 55.5%; Pred. No. 4.9e-81;  
Matches 776, Complement 0, Mismatches 506; Indels 117; Gaps 3;

QY 380 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 149  
Db 314 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 149  
QY 440 ATGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 373  
Db 374 ATGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 373  
QY 500 CTGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 499  
Db 434 ATGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 499  
QY 560 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 619  
Db 494 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 619  
QY 620 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 679  
Db 554 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 679  
QY 680 ATGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 739  
Db 614 ATGCTGGCTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 739  
QY 740 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 799  
Db 674 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 799  
QY 800 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 859  
Db 734 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 859  
QY 860 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 919  
Db 794 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 919  
QY 920 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 979  
Db 853 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 979  
QY 980 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1039  
Db 853 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1039  
QY 1040 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1099  
Db 878 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1099  
QY 1100 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1159  
Db 926 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1159  
QY 1160 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1219  
Db 983 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1219  
QY 1220 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1279  
Db 1043 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1279  
QY 1280 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1339  
Db 1103 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1339  
QY 1340 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1399  
Db 1163 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1399  
QY 1400 GGAACCACTGCTGCTGGAAGTCTGATTAATGCTGAGTAAATGCTATGAGGAGAGGG 1459

RESULT 10  
US-09-776-705-1.rnpb  
Sequence 30420, Application US/09864761  
Patent No. US2004084761A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon D.  
INVENTOR: Penn, Sharon D.  
APPLICANT: Penn, Sharon D.  
INVENTOR: Penn, Sharon D.  
TITLE OF INVENTION: HUMAN GENE  
FILE REPRESENTATIVE: X-1  
CURRENT APPLICATION NUMBER: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/180,412  
PRIOR FILING DATE: 2001-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 60/632,406  
PRIOR FILING DATE: 2000-06-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687









Best local Similarity 1.00%; Prod. No. 1.25-093

Matches 6; Conservative 242; Mismatches 148; Indels 0; Gaps 0.

```

QY 4 TTTAAATAGTACAGAAATCTGACAGACTGATTAATTAATTAAGAGAGATGCTTC 63
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1457 TACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1478
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 64 TGAATATATATATATATATATATATATATATATATATATATATATATATAT 124
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1377 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1418
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 124 AAGAGATATATATATATATATATATATATATATATATATATATATATATAT 184
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1217 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1258
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 184 AATATATATATATATATATATATATATATATATATATATATATATATAT 243
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1257 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1198
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 244 CATATATATATATATATATATATATATATATATATATATATATATATAT 304
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1197 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1148
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 304 TAAAGATATATATATATATATATATATATATATATATATATATATATAT 364
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1137 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1078
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 364 TATATATATATATATATATATATATATATATATATATATATATATATAT 479
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1077 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1062
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RESULT 2

US-08-242-464-14

Sequence 14, Application US/08/242-464

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DERNER, F.

APPLICANT: SCHIEFFELINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT POWDERX VIRUS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Hardner

STREET: 1800 diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22312-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/242-464

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,413

FILING DATE:

APPLICATION NUMBER: IT 91 114 300.6

FILING DATE: 26-AUG-1991

AUTOPREPARATION: YES/NO: N

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

TELECOMMUNICATIONS: 204,223,114 (2007)

TELEPHONE: (703) 846-9300

TELEFAX: (703) 843-4109

TELEX: 899149

INFORMATION: YES/NO: N

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs  
 TYPE: nucleic acid  
 STRATEGY: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: pTZapt-Fls  
 US-08-232-464-14

Query Match: 3.0%; Score 55.2; DB 1; Length 7218;

Best Local Similarity: 4.5%; Prod. No. 24 067;

Matches 18; Conservative 221; Mismatches 159; Indels 0; Gaps 0;

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QY 1274 TGCATGACGGGACGATCTGTCATGTACATGCTGTGGGACCTCTCTGCTTACCTAACTTC 1388
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1044 TCCAGATGAGGAGACCTGCGATATATATATATATATATATATATATATAT 1108
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1344 TATATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1104 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1164
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1394 CTTCTTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1164 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1228
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1454 CTTCTTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1518
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1224 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1288
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1514 ATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1284 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1348
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1574 GTCATGACGGGACGATCTGTCATGTACATGCTGTGGGACCTCTCTGCTTAC 1638
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1344 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1408
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 1634 TTTATCTTTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1671
  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1404 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1468
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RESULT 4

US-08-484-101B-41

Sequence 11, Application US/08/484101B

Patent No. 5824868

GENERAL INFORMATION:

APPLICANT: California Institute of Technology

TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO

TITLE OF INVENTION: ETHYLENE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Trancartin

STREET: 4400 Emburyadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,101B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 800

TELECOMMUNICATIONS DATA:

TELEPHONE: 301,953,417

TELEFAX: 01-JUL-1994

TELEX: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/086,555

FILING DATE: 01-JUL-1994









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: Sequence 1780, Application US/09134001C
: Patent No. 6460576
: GENERAL INFORMATION:
: APPLICANT: Lyda Boucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
: TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: G1C-007
: CURRENT APPLICATION NUMBER: US-09/034,001C
: CURRENT FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/095,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ IN SET: 5674
: SEQ ID NO 1780
: LENGTH: 616
: TYPE: DNA
: ORGANISM: Staphylococcus epidermidis
: US-09-134-001C-1780

Query Match      1.9%; Score 35.4; DB 4; Length 816;
Best local similarity 56.4%, E-val. 0.0%;
Matches 66; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

787 AATTATTCTTCACGCTTCCTGCTTCAAAAATTTAGGTTTATCTTGCTATACACAGTGATTT 846
298 AATGAGGCTGCTGAGCTGCTGCTTTCAGAAATATTTTCACCAATTATGACGACCCAGAAAT 357
847 TCTCTTACGTCGAGGAGGCTTTTCTGAGTGGTGATTTACAGAAATTCCTCAAT 903
358 ACTTTATAGTCGAGGAGGAACTTACCTTATGATGCTGATTTAGAAACAATTAGATAT 414

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RESULT 14  
 US-09-149-476-216/c  
 Sequence 216, Application US/09149476  
 Patent No. 6420526  
 GENERAL INFORMATION  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: 160 human secreted proteins  
 FILE REFERENCE: P200201  
 CURRENT APPLICATION NUMBER: US/09/149,476  
 EARLIER FILING DATE: 1998-09-08  
 EARLIER APPLICATION NUMBER: EC/US98/04453  
 EARLIER FILING DATE: 1998-03-06  
 EARLIER APPLICATION NUMBER: 66/040,152  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/040,333  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/038,621  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/040,626  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/040,354  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 66/040,336  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/040,163  
 EARLIER FILING DATE: 1997-03-07  
 EARLIER APPLICATION NUMBER: 60/047,000  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 66/041,615  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,597  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/041,502  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 66/047,033  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,583  
 EARLIER FILING DATE: 1997-05-23  
 EARLIER APPLICATION NUMBER: 60/047,617  
 EARLIER FILING DATE: 1997-05-23



QY 1575 TGGCACTATAAAATACATCTCGGATTCATAGGGCTCTCTCTCGCACTATGCGTATTT 1634  
Db 1412 TGGNTAYYTNATGGAYYNTTYMGNTGCAAGCTNTTYCAYGSHACNATHGGAARGAYA 1471  
QY 1635 TTATCTCTCACCAGCTTTTATGCTTAAAGCTTGTCAGAGAAAGAACTTLAGGTCAGCCC 1694  
Db 1472 THTAYAYCARGARTGGTGGAAAYTNMGNMGNNTNAARTAYCARGSNYTNTRYCCNCA 1531  
QY 1695 AAAAGGTCGGGCTTTAAATTTCTCTGTGGTTGGAATATCTTCATGATTTGGAAGCATGG 1754  
Db 1532 THCCNCAYWNGARGARGAYTTYGAYCGGNGGNCNAARTTYCAVTTYWSNCGNGGCTNC 1591  
QY 1755 CACTCATTAATGACTGGATTTAIGATCCTCGAAATTCGAAGCATCAGTAA 1807  
Db 1592 CNTAYATHCHRGNTAYTTYTNWGNNTNGTNYTNCARTTYCARTTYCAYGAR 1644

Search completed: January 4, 2003, 15:11:32  
Job time : 246.153 secs





ER W:200106146\_A2.  
 XX 29-NOV-2001.  
 XX 17-MAY-2001; 2001W-05161019.  
 XX 19 MAY 2003; 2003W-2002004.  
 XX (MILL.) MILDENHIRE PHARM INC.  
 XX CURTIS RAD;  
 XX KPI3; 2002-084084/11  
 XX P-PSDB; AMB09219.  
 XX  
 PI New membrane transporter protein (referred to as 57256 and 58289),  
 PI useful for diagnosing, treating disorders e.g. Alzheimer's disease  
 PI mania, obsessive-compulsive disorder, anxiety and diabetes.  
 XX  
 PS Claim 1: Fig 4: 14pp; English.  
 XX  
 SC The sequence encodes human membrane transporter protein 58289. The  
 SC invention relates to novel isolated membrane transporter protein (58289)  
 SC polypeptides, (referred to as 57256 and 58289). The polypeptides of the  
 SC invention have neurotropic, neuroprotective, anti-Alzheimer's disease,  
 SC anticonvulsant, neuroleptic, antidepressant, anxiolytic, tranquilizer,  
 SC antimigraine, anorectic, antihypertensive, vasorelaxant, cardiac,  
 SC antitumoral, antiarrhythmic, cytostatic, antitumor, and immunostimulant  
 SC activity. The polypeptides are polypeptides having a size in gene  
 SC therapy, and act as modulators of the protein or nucleic acid, and as  
 SC transcription and/or translation inhibitors. Both the polypeptide and  
 SC polynucleotide are useful as modulation agents in regulating cellular  
 SC process e.g. cellular proliferation, growth, differentiation, or  
 SC migration, which is useful in treatment and diagnosis of transporter  
 SC associated disorders. These disorders include central nervous system  
 SC (CNS) disorders, autoimmune function disorders, learning or memory  
 SC disorders, bipolar affective neurological disorders, cardiac related  
 SC disorders, cancer, tumor angiogenesis and metastasis, skeletal  
 SC dysplasia, hepatic disorders, hematopoietic and/or myeloid disorders,  
 SC disorder, hormonal disorders, and immune disorders. The polypeptides and  
 SC polynucleotides, and homologues of the polynucleotides and antibodies,  
 SC are useful for screening assays, predictive medicine (e.g. diagnostic  
 SC assays, prognostic assays, monitoring clinical trials, and  
 SC pharmacogenetics) and treatment (e.g. therapeutic and prophylactic).  
 XX  
 SQ Sequence 3767 bp; 1157 A; 713 C; 690 G; 1207 T; 0 other;

Query Match 98.1%; Score 1787.2; DB 24; Length 3767;  
 Best Local Similarity 99.6%; Prod No. 0;  
 Matches 1792; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
 QY 23 GCTGTCACAGAGCTGGATATAATTAAGAACAGAGTGTCTGAAATATTAACACAAAGTG 82  
 DB 18 GCTGTCACAGAGCTGGATATAATTAAGAACAGAGTGTCTGAAATATTAACACAAAGTG 77  
 QY 83 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 142  
 DB 78 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 147  
 QY 143 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 202  
 DB 148 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 197  
 QY 203 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 262  
 DB 198 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 257  
 QY 263 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 322  
 DB 258 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 317  
 QY 323 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 382  
 DB 318 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 387

118 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 437  
 QY 483 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 442  
 DB 478 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 437  
 QY 443 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 502  
 DB 448 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 497  
 QY 503 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 562  
 DB 498 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 557  
 QY 563 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 622  
 DB 558 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 617  
 QY 623 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 682  
 DB 618 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 677  
 QY 683 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 742  
 DB 678 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 737  
 QY 743 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 802  
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 QY 803 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 862  
 DB 798 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 857  
 QY 863 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 922  
 DB 858 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 917  
 QY 923 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 982  
 DB 918 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 977  
 QY 983 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1042  
 DB 978 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1037  
 QY 1043 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1102  
 DB 1038 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1097  
 QY 1103 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1162  
 DB 1098 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1157  
 QY 1163 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1222  
 DB 1158 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1217  
 QY 1223 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1282  
 DB 1218 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1277  
 QY 1283 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1342  
 DB 1278 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1337  
 QY 1343 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1402  
 DB 1338 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1397  
 QY 1403 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1462  
 DB 1398 AAGAAATCTTAAGATGAAAGTAAAGTAAATATTAATTAATTAATTAATTAATTAATTA 1457







The invention relates to human transporters and ion channels (TRICP) polypeptides and their cDNA molecules, the nucleic acid and polypeptide sequences are useful in the diagnosis, treatment, and prevention of disorders associated with transport (akinesia, cystic fibrosis, Bell's palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease, amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's muscular dystrophy); immunological (AIDS, Addison's disease, allergies, asthma); cell proliferative disorders (cancers, leukemias, psoriasis); cardiac (angina, hypertension, or bradyarrhythmia) and in the assessment of the effects of xenobiotics compounds on the expression of nucleic acid and amino acid sequences of transporters and ion channels. The polynucleotides may be used to detect and quantify gene expression in biosized tissues in which TRICP expression may be correlated with a disease, to generate hybridization probes for mapping naturally occurring genomic sequence, and in drug screening. The present sequence is human TRICP-19 cDNA.

Source 2074 BL; 583 A; 421 C; 491 G; 475 F; 4 other;

Query Match 65.18; Score 1185.8; PB 24; Length 2074;

Best local similarity 88.0%; Prod. No. 0;

Matches 1862; Conservative 47; Models 138; Goss 1;

QY	276	AGAGAAATGCAATTTGTTAAATGAAGACATGAAAGATGCAAAATTTGCAAAATGAATTTT	430
DB	459	TTTTCAGTCAATTTGTTTAAAGAGACATGAAGATTTGCAAAATTTGCAAAATGAATTTT	518
QY	136	TGAGGAAAAAATATGAGAAATTAATTTGATGAGAAATGATGATGAAATGATTTGCTTTC	495
DB	519	TGGAAAAAAGATGAGCAATGCTTCTTTTAAAGATGCAAGAAATGCTTCTTTC	578
QY	396	GAATGTTTTCATTTAACTTGAATTAATGATCATGAGGACATGGGATCTGAGCTTGTCTCT	455
DB	579	GAATGTTTTCATTTAACTTGAATTAATGATCATGAGGACATGGGATCTGAGCTTGTCTCT	638
QY	456	ATGCAATGAGCTATACAGAGAGTTCATCTTTTATAATATGATGCTTGTGTTGGCAATAT	513
DB	649	ATGCAATGAGCTATACAGAGAGTTCATCTTTTATAATATGATGCTTGTGTTGGCAATAT	698
QY	516	TATTACTGTTATPAGTTTAACTTTTATTAATAAAATAGTAAAGAAAGAACTTTTGATTT	575
DB	699	TATTACTGTTATPAGTTTAACTTTTATTAATAAAATAGTAAAGAAAGAACTTTTGATTT	758
QY	576	ATGAAAAATATAGAAAGAAATGATGATGAGGAGAAAAATATGAGCTTTTGTTTGCA	635
DB	759	ATGAAAAATATAGGAGAAAAAGATTTGATGAGGAGAAAAATATGAGCTTTTGTTTGCA	818
QY	646	TTAATAAGTAATATGAGTAAGTGAAGTACCTTTTATCATTAATAATATGAATATAC	695
DB	819	TTAATAAGTAATATGAGTAAGTGAAGTACCTTTTATCATTAATAATATGAATATAC	878
QY	696	TTGAGTAATATGAGTAATATGAGTAATGAAAAAATATGAAAAATGATGATTTCAATG	755
DB	879	TTGAGTAATATGAGTAATATGAGTAATGAAAAAATATGAAAAATGATGATTTCAATG	938
QY	756	GAATATACATCATATATTTGCTGTGTGTGAAATATGCTGATTTTGTCTTTTAAAA	815
DB	949	GAATATACATCATATATTTGCTGTGTGTGAAATATGCTGATTTTGTCTTTTAAAA	998
QY	816	ATTATAGTATCTGGTATATACATGCAATTTCTGCTTATCTGATGCTGCTTTTGTCTA	875
DB	999	ATTATAGTATCTGGTATATACATGCAATTTCTGCTTATCTGATGCTGCTTTTGTCTA	1058
QY	876	ATCTGCTGATTTAAAGAAATGAAAAATAGCTGCTGCTGCTGCTTTTAAATACATG	945
DB	1059	ATCTGCTGATTTAAAGAAATGAAAAATAGCTGCTGCTGCTGCTTTTAAATACATG	1101
QY	946	TTGAAAACTGCTATTCATCAATACATGATTTGTAATGATGAGTGAATGATGATGCAACT	995
DB	1102	TTGAAAACTGCTATTCATCAATACATGATTTGTAATGATGAGTGAATGATGATGCAACT	1101
QY	996	CTGAAATCTTGAGATGAATTTTATGATGATTAATTAATGATGATGATGATGATGATG	1055







AA034664 standard; cDNA: 2320 bp.	XX
AA034664;	XX
01-JUL-2002 (first entry)	XX
Human TRICH-10 cDNA.	XX
human; transporter and ion channel; TRICH-10; transport disorder; anion; ankyrotic lateral sclerosis; cystic fibrosis; neuromuscular disease; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer; depression; schizophrenia; aneurism; Wilson's disease; Cushing's disease; cell proliferated disorder; infertility; arteriosclerosis; bone disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy; myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension; acquired immune deficiency syndrome; immunological disorder; autoimmune disorder; autoimmune thyroiditis; rheumatoid arthritis; polycystic cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection; epilepsy; mental disorder; myocarditis; cerebral disease; Graves' disease; muscle disorder; stroke; pneumonia; aneurism; AIDS; asthma; encephalitis; gene; SS.	XX
Homo sapiens.	XX
CS	XX
KW	XX
LOCUS: 400424; 400425	XX
375,11895	XX
2433	XX
/product: "human TRICH-10 protein"	XX
W020021240-A2.	XX
14-FEB-2002.	XX
01-AUG-2001: 2001W-0524217.	XX
03-AUG-2000: 2000MS-223269P.	XX
10-AUG-2000: 2000MS-224156P.	XX
18-AUG-2000: 2000MS-224610P.	XX
25-AUG-2000: 2000MS-228143P.	XX
31-AUG-2000: 2000MS-240067P.	XX
08-SEP-2000: 2000MS-24144P.	XX
(INV-) INYTE GENOMICS INC.	XX
Yao H, Thornton M, Kankumar T, Tang YL, Azimov A, Koshin M, Yang J, Yao MS, Lai P, Walla NS, Gandhi AP, Hattalia AA, Ruyun DB, Patterson C, Elliott VS, Trishinsky CM, Lu DM, Xu Y, Kody B, Hernandez K, Borozsky ML, Lo TP, Lu Y, Policky JL, Greene BD, Sanjanwalla MS, Kaumann DE, Burford N, Yoon CH, Lee EA, Ding L, Das D, Kallik DM, Khan BA, Seilhamer JJ;	XX
WPI: 2002-206330/26.	XX
P-PSDB: AA021174.	XX
New human transporters and ion channels polypeptides and polynucleotides for diagnosis, prevention of treating transport, neurological, muscle, immunological and cell proliferative disorders	XX
claim 92: Page 217-218: 230pp. English.	XX
The invention relates to human transporter and ion channel polypeptides designated TRICH and nuclear acid molecules encoding such polypeptides. TRICH sequences are useful for diagnosis, treatment and prevention of transport, muscle, neurological, immunological and cell proliferative disorders. Transport disorders include ataxia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis, myocarditis, prostate cancer, cardiac disorders associated with transport e.g. polymyositis, bradyarrhythmia, dermatomyositis, anion, neurological disorders associated with transport e.g. amnesia, bipolar disorder, depression, ionocyte's disorder, schizophrenia, other disorders associated with transport e.g. neurofibromatosis, stroke, cell anaemia, Wilson's disease, epilepsy, fibrotic, hypertrophic cardiomyopathy, myasthenia,	XX

XX	Human: breast cancer; cell marker; cytosolatic; ss.
KW	Human sapiens.
OS	W0200151428-A2.
PN	19-JUL-2001.
PD	10-JAN-2001; 2001WO-0500798.
PF	14-MAR-2000; 2000US-0176077.
PR	14-MAR-2000; 2000US-0189167.
TR	23-MAR-2000; 2000US-0192099.
FE	23-MAR-2000; 2000US-0194480.
PR	15-MAY-2000; 2000US-0205240.
PR	09-JUN-2000; 2000US-0211315.
XX	25-JUL-2000; 2000US-0220534.
PA	(MILLI-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	Lillie J, Xu Y, Wang Y, Steinmann K;
XX	W01; 2001-451856/48.
DR	New peptide useful as a marker for the diagnosis of breast cancer
PT	Claim 1; Page 986; 4695pp; English.
PS	The invention relates to human breast cancer expressed polynucleotides
CC	(AA107544-AAL26789) and methods of assessing whether a patient is
CC	afflicted with breast cancer by examining the correlation between the
CC	expression of certain markers and the cancerous state of breast cells.
CC	The polynucleotides and encoded polypeptides are potential markers for
CC	detecting, diagnosing, predicting, evaluating, and/or treating cancer
CC	potentially preventing breast cancer; the polynucleotides and encoded
CC	polypeptides are also useful for isolating compounds with cytostatic
CC	activity.
XX	Sequence 548 BP; 172 A; 100 C; 140 G; 136 T; 0 other;
QY	Query Match 25.18; Score 457; DB 22; Length 548;
DB	Post. local similarity 36.28; Ident. No. 4; seq-124;
DB	Matches 501; Conservative 9; Mismatches 15; Indels 5; Gaps
102	GTACAGTAATATTATTCACCTGAGGGGCTGTGTGTGGACAGAAAGGCTGATACCTT 161
23	GCACAGTAATATTATTCACCTGAGGGGCTGTGTGTGGACAGAAAGGCTGATACCTT 82
162	AAATGGATCTCATCTGACATGAGAATGTCAACATGCAAGTCAATGATGAGAGACATP 221
83	AAATGGATCTCATCTGACATGAGAATGTCAACATGCAAGTCAATGATGAGAGAGAG 142
222	CAGAAATGCTGTCAGATAGCTACATGAGATAGAAATTCAGAAAAAGTCAGCAATCA 281
143	GAGAAAGTCTCTCAGATAGCTACATGAGATAGCAATTCAGAAAAAGTCAGCAATCA 202
232	CTCAATTTCTTAATGAAGACACTGAAAGTCAGAAATTCCTGCAATATTCCTGCA 41
203	GTCATTTCTTAATGAAGACACTGAAAGTCAGAAATTCCTGCAATATTCCTGCA 262
342	AAAAGAGTCTGTCAGATATGCTGATGAGACATCATCTCTGCAAGCAATTCCTTGA 401
263	AAAAGAGTCTGTCAGATATGCTGATGAGACATCATCTCTGCAAGCAATTCCTTGA 322
402	CTTCATTTATGCTCAATTAAGGCAATGATGAGAGAGAGATCTGCTGCTGCTGCTG 461
323	CTTCATTTATGCTCAATTAAGGCAATGATGAGAGAGAGATCTGCTGCTGCTGCTG 482
462	TGGATCACAAGGGGTCATACCTTTTATATCATGCTGCTGCTGCTGCTGCTGCTGCT 521
384	TGGGCAACACAGGTCATACCTTTTATATCACAAGGTCCTGCTGCTGCTGCTGCTGCT 442





[illegible]





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 00:30:55, Search time 761.44 seconds  
(without alignments)  
10634.887 Million cell updates/sec

Title: US-09-776-705-3\_cofy\_l\_500

Perfect score: 500

Sequence: 1 agcttaacataatgatcaaa.....ataatcaaaaataaactaaa 500

Scoring table: IDENTITY:NUC  
Gapop 10.0, Gapext 1.0

Search-d: 1615000 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32368142

Minimum DB seq length: 0

Maximum LB seq length: 10000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST

1: em\_estba: \*  
2: em\_estbam: \*  
3: em\_estin: \*  
4: em\_estin: \*  
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6: em\_estov: \*  
7: em\_estov: \*  
8: em\_estov: \*  
9: gb\_est1: \*  
10: gb\_est1: \*  
11: gb\_est1: \*  
12: gb\_est1: \*  
13: gb\_est1: \*  
14: gb\_est1: \*  
15: em\_estin: \*  
16: em\_estin: \*  
17: gb\_gss: \*  
18: gb\_gss: \*  
19: em\_gss: \*  
20: em\_gss: \*  
21: em\_gss: \*  
22: em\_gss: \*  
23: em\_gss: \*  
24: em\_gss: \*  
25: em\_gss: \*  
26: em\_gss: \*  
27: em\_gss: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.6	12.2	101	CNS01219	AL101595 Drosophil
2	63.6	12.7	945	CNS0460K	AL285149 Tetraodon
3	60	12.0	576	CNS035N7	AL228940 Tetraodon
4	59.4	11.9	1131	CNS002F3	AL062437 Drosophil
5	59.4	11.9	1101	CNS006VL	AL069706 Drosophil
6	58.4	11.7	974	CNS001IT	AL075432 Drosophil

C	7	58.2	11.6	424	17	CNS000R0N
C	8	58	11.6	1101	17	CNS000390
C	9	57.2	11.4	1006	17	CNS010EY
C	10	56.6	11.3	759	17	CNS000490
C	11	56.6	11.2	1101	17	CNS0008XV
C	12	56.2	11.0	945	17	CNS0008XV
C	13	55.2	10.9	725	17	BH180166
C	14	54.4	10.9	956	17	CNS000F0H
C	15	53.6	10.7	1101	17	CNS000B0I
C	16	53.4	10.7	950	17	CNS0006LM
C	17	52.8	10.6	750	17	CNS0111D
C	18	52.6	10.5	879	17	CNS01JRG
C	19	52.6	10.5	978	17	CNS000KV3
C	20	52.4	10.5	660	17	BH183498
C	21	52.4	10.5	660	17	CNS0008XV
C	22	52.4	10.5	660	17	CNS0008XV
C	23	52	10.4	480	17	BH183714
C	24	52	10.4	753	17	CNS000A1S
C	25	52	10.4	1141	17	CNS014A0
C	26	52	10.4	1184	17	CNS004D4P
C	27	51.8	10.4	1101	17	CNS000390
C	28	51.4	10.3	655	17	CNS01700
C	29	51.3	10.3	812	17	CNS000625
C	30	51.2	10.2	878	17	CNS0187K
C	31	51.2	10.2	945	17	BH180831
C	32	51.2	10.2	1201	17	CNS0161H
C	33	51	10.2	1167	17	CNS00750
C	34	50.8	10.2	529	9	AL514657
C	35	50.8	10.2	793	17	CNS011BP
C	36	50.8	10.2	963	17	CNS007EBK
C	37	50.6	10.1	1035	17	CNS0155H
C	38	50.6	10.1	945	13	BH558135
C	39	50.6	10.1	1131	17	CNS0106X
C	40	50.6	10.1	1134	17	AG057537
C	41	50.6	10.1	1201	17	CNS0167M
C	42	50.4	10.1	994	17	CNS004NOJ
C	43	50.4	10.1	1101	17	CNS003HD
C	44	50.2	10.0	816	17	CNS02K4V
C	45	50.2	10.0	1201	17	CNS0103V

## ALIGNMENTS

CNS01219 1101 bp DNA linear GSS 26-JUL-1999  
Drosophila melanogaster genome survey sequence Sp6 end of RAC  
BAC28524 of Drosophila library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
AL101595  
GSS.  
AL101595.1 G1:5613206  
Drosophila melanogaster.  
Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Protopoda;  
Ephryptera; Eudopterygota; Diptera; Brachycera; Muscomorpha;  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (26-JUL-1999) Genoscope - Centre National de Sequencage  
RP 191 01006 EVRY cedex - FRANCE (E-mail : seqref.genoscope.cns.fr)  
Web : www.genoscope.cns.fr  
collaboration with the European Drosophila Genome Project (DEP)  
Library (GSS-BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
Project grant. The BAC was prepared from colonies by Alain Bouchon  
and Genoscope payan. It has been subcloned in the vector  
pBluescript.

## FEATURES

Location/Qualifiers

















10 855 WWTAWTAAAAATYAAATTTAAAWITWAWA 882

Search completed: January 4, 2003, 12:30:55  
Job time : 769.432 secs







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00  82712 TTTCACAAATGAAGCAACTACAAATTCATTATACA 82747
      11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 8
US-09-960-352-15014/c
? Sequence 15014, Application US/09/960352
? Patent NO. US20020137149A1
? GENERAL INFORMATION:
? APPLICANT: Warren, Wesley C.
? APPLICANT: Tac, Ronald
? APPLICANT: Beatt, John C.
? APPLICANT: Bachalaram, Narappa
? TITLE OF INVENTION: BOTTLE ACID AND OTHER MEMBRANE ASSOCIATED WITH CAPSULATION AND
? TITLE OF INVENTION: BOTTLE AND FILL DECONTAMINATION
? FILE REFERENCE: 16511.006/47 21(10258)
? CURRENT APPLICATION NUMBER: US09/960352
? CURRENT FILING DATE: 2001-09-24
? NUMBER OF SEQ ID NOS: 15112
? SEQ ID NO 15014
? LENGTH: 375
? TYPE: DNA
? ORGANISM: Bos taurus
? OTHER INFORMATION: Clone ID: 64-11B3058-048-Q1-K1-B8
US-09-960-352-15014

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Query Match	8.3%	Score 41.47	DB 10	Length 440
Best Local Similarity	59.2%	Prod. No. 2.7		
Matches 129	Conservative 0	Mismatches 126	Indels 1	Gaps
QY 212	ATGAAAGAAAGAGATAAAATCTGGAATCTTCAGAAAACATGATATAATATCTATTA	271		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 414	ATATAAAAATATATAAAAATATATAAAAATATATAAAAATATATAAAAATATAT	456		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 272	AACAAATAAAGAGAGATCAATATAGAGATATAGAGATATATCTTCATCAATCTC	341		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 354	AGAGAGAGAT	295		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 332	GAGAGAGAGATATCTGGAATCTAGAAATTCAGAAATATATATATATATATATAT	490		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 294	GAGAGAGAGAGAT	245		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 351	AACAAATAAAGAGAGATCAATATAGAGATATAGAGATATATCTTCATCAATCTC	450		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 254	AGAGAGAGAT	175		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 451	GAGAGAGAGAT	465		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			
QY 174	TAGAGAGAGAT	160		
140	111 111 111 111 111 111 111 111 111 111 111 111 111 111			

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1  RESULT 9
2  US-09-960-253-0197-0
3  ? Sequence 5818, Application 09/0960452
4  ? Patent No. 6509060 (200309A)
5  ? GENERAL INFORMATION:
6  ? APPLICANT: Warner, Wesley C.
7  ? APPLICANT: Iaso, Nandiniq
8  ? APPLICANT: Ryatt, John C.
9  ? APPLICANT: Mathulalan, Nandapab
10 ? TITLE OF INVENTION: NOCTE ACID AND OTHER PEPTIDES ASSOCIATED WITH LACTATION AND
11 ? TITLE OF INVENTION: NOCTE ACID AND OTHER PEPTIDES ASSOCIATED WITH LACTATION AND
12 ? FILE REFERENCE: 16511.006/47-21(10298)C
13 ? FILE REFERENCE: 16511.006/47-21(10298)C
14 ? CURRENT APPLICATION NUMBER: US/09/960,452
15 ? CURRENT FILING DATE: 2001-09-24
16 ? NUMBER OF SEQ. ID NOS.: 1011
17 ? SEQ. ID NO 5818
18 ? LENGTH: 430
19 ? TYPE: DNA
20 ? ORGANISM: Bos taurus
21 ? OTHER INFORMATION: Clone ID: 25 LIB3058-011-Q1-K1-09

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[illegible]

[illegible]

RESULT 13  
JS 09 960 352-7166/c  
: Sequence 7196, Application US/09960352  
: Patent No. US20020137139A1

RESULT 12  
US-09-960-252-2400/C  
: Sequence 3400, Application US/07990352  
: Patent No. US20020137139A1

TYPE: DNA  
ORGANISM: Bos taurus  
CLONE INFORMATION: Name: Bp. 27, 1 kb, 5' end of A1 H3  
US-09-960-352-7186

[illegible]

RESULT 14  
US-09-867-701-7175  
; Sequence 7175, Application US/09867701  
; Patent NO. US2,620,3237A1  
; GENERAL INFORMATION:

RESULT 14  
US-09-867-701-7175  
; Sequence 7175, Application US/09867701  
; Patient No. US20132237A1  
; GENERAL INFORMATION:











NAME: Quine, Jonathan A.  
 REGISTRATION NUMBER: P-41,261  
 REFERENCE/DECKT NUMBER: 023076 07210005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1177 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 1..1177  
 OTHER INFORMATION: /note= "tomato acidic leucine  
 aminopeptidase 2 (LapA2) promoter  
 region"  
 US-08-892-770-3

Query Match  
 Best Local Similarity: 55.7%, Freq. No. 9.9,  
 Matches: 73; Conservative: 0; Mismatches: 58; Indels: 0; Gaps: 0  
 QY 295 AATAGAGCTAGAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 354  
 Db 251 AAATAAGAGAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 310  
 QY 355 GAATTCACCAATTAACCAAGTTTGAAGGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 414  
 Db 311 AAATGAGAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 370  
 QY 415 TCAGAAATTCCT 425  
 Db 371 AAGAGAGAGAGAGTTTC 381

RESULT 9  
 US-09-056-075-1  
 Sequence 1: Application US/09056075  
 Patent No. 5955368  
 GENERAL INFORMATION:  
 APPLICANT: Johnson, Eric A.  
 APPLICANT: Bradshaw, Marite  
 APPLICANT: Reed, Julian  
 TITLE OF INVENTION: Expression System for Clostridium  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quigley & Brady  
 STREET: 1 South Pinckney Street  
 CITY: Madison  
 STATE: WI  
 COUNTRY: US  
 ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-056-075  
 FILING DATE:  
 CLASSIFICATION:  
 ATORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27386  
 REFERENCE/DECKT NUMBER: 023076 052208  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166  
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 6243 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 3770..4013  
 OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from  
 plasmid RP4"  
 US-09-056-075-1

Query Match  
 Best Local Similarity: 7.68%, Score 37.8; DB 2: Length: 6243;  
 Matches: 127; Conservative: 0; Mismatches: 127; Indels: 3; Gaps: 1;  
 QY 212 ATAGAGCTAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 271  
 Db 1183 ATAGAGCTAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 1242  
 QY 272 AATAGAGCTAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 328  
 Db 1243 AATAGAGCTAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 1402  
 QY 229 TCAGAAATTCCT 245  
 Db 1303 TAAAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 388  
 QY 389 TAAAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 448  
 Db 1363 AATAGAGAGAGAGAGTTTCATATTCGTGAAGGAGAAATGCTTCGATCTA 1422  
 QY 449 GTCAAGAGAGAGTTTC 465  
 Db 1423 TGAAGAGAGAGTTTC 1439

RESULT 10  
 US-09-014-969-14  
 Sequence 1: Application US/09014969  
 Patent No. 5965367  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, Kenneth  
 APPLICANT: McCoy, John M.  
 APPLICANT: Lavallee, Edward R.  
 APPLICANT: Kach, Lisa A.  
 APPLICANT: Mcberg, David  
 APPLICANT: Treacy, Maurice  
 APPLICANT: Spaulding, Vikki  
 APPLICANT: Apostol, Michael J.  
 TITLE OF INVENTION: SECRETED PROTEINS ARE POLYNUCLEOTIDES  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 Cambridgeport Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: U.S.A.  
 ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-014-969  
 FILING DATE:  
 CLASSIFICATION:  
 ATORNEY/AGENT INFORMATION:  
 NAME: Spurgeon, Suzanne A.  
 REGISTRATION NUMBER: 41323





DB 1477 CTTGTAATATGTAATAAAGAAATTTACTGATCTTCTCAAAATCAATGTTGCAAAAGGATAG 2036

QY 271 AAGCAAAATATAGAGGAGAG 287

DB 2037 TGAAGGACAGAGAGGAG 2053

# RESULT 15

US-08 920-812-6

: Sequence 6, Application US/08920812

: Patent No. 5763188

: GENERAL INFORMATION:

: APPLICANT: Chono, Tsuneyu

: APPLICANT: Matsushima, Akio

: APPLICANT: Uehara, Hirotsugu

: APPLICANT: Eda, Soji

: TITLE OF INVENTION: Probe for Diagnosing Infectious Disease

: NUMBER OF SEQUENCES: 25

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Marshall, O'Toole, Gorsteln, Murray & Borum

: STREET: 6400 Sears Tower, 233 South Wacker Drive

: CITY: Chicago

: STATE: Illinois

: COUNTRY: United States of America

: ZIP: 60606-6402

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/920,812

: FILING DATE: 29-AUG-1997

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 09/462,577

: FILING DATE: 27-MAR-1995

: ATTORNEY/AGENT INFORMATION:

: NAME: Rin-Lauros, Li-Hsien

: REGISTRATION NUMBER: 34,547

: REFERENCE/SEQUENCE NUMBER: 19036/32320

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 312/474-6300

: TELEFAX: 312/474-0448

: TELEX: 25 8856

: INFORMATION FOR SEQ ID NO: 6:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 8654 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: genomic DNA

: ORIGINAL SOURCE:

: ORGANISM: Staphylococcus epidermidis

: STRAIN: Clinical Isolate SE-22

US-08 920-812-6

## Query Match

Best Local Similarity 52.28; Pred. No. 2.7; Score 47; DB 1; Length 8654;

Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 261 AATTATCTATAAAGAAATATAGAGGAGAGTCTATTAATAGAAATAGAGAGAGGAGG 320

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

DB 2293 AATTTCTTAAATTAATAAATAATATAAATAAATAAATAAATAAATAAATAA 2352

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

QY 421 TTCAATATCTGAGGAGAGAGGCTCTGAGAGTCTAGAGATTAATAAATAAATAA 380

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

DB 2353 TAACATTTTATATAAAGAGTCTATTAATTAAGAGTAGAGATTTTAAACTTTTC 2412

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

QY 481 AGGCAAAATATAGAAATTTCTCAATCAATGAGAGAGGAGG 417

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

DB 2413 ATCTATCAATAAGCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 2449

||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

Search completed: January 4, 2003, 15:12:05  
Job time : 56.917 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on: January 4, 2002, 10:57.01
Search time 109.50/ seconds
(without alignments)
1022.476 Million cell updates/sec
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Title: US-09 776-705 3 COFY 1 500

Perfect score:

Sequence: 1 ap<sup>0</sup>1tagcaataggatca.....atadtgcacaa13aaactgaa 500

Scoring table: IDENTITY NIT

Gapex 10.0 , Gapext 1.0

Searched: 2186239 exp, 12239113, 1364125

Parameter	Value
Total number of hits satisfying chosen parameters.	4376478

Minimum DB seq length: 0

Maximum DB seq	length: 2000000000
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Post-processing: Minimum Match 0.9

Maximum Match 100%

Listing first 45 summaries

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result	No.	Score	Query		Length	DB	ID	Description	
			Match	%					
C	1	52.4	10.5	3742	24	ABL70680		Chemically treated	
C	2	51.4	10.3	38342	22	AAS46746		Tumour suppressor	
C	3	51.4	10.3	38742	24	ABK21597		Signal transductor	
C	4	50.8	10.2	15674	24	ABL710514		Chemically treated	
C	5	50.8	10.2	15674	24	ABL323363		Human immune syste	
C	6	50.8	10.2	15674	24	ABL334777		Human metastasis a	
C	7	49.6	9.9	5946	24	AAS61400		Human gene regulat	
C	8	49	9.8	6089	22	ABL16580		Tumour suppressor	
C	9	49	9.8	6089	24	ABL34837		Human immune syste	

## ALL COMMENTS

## RESULT 1

# CONSTITUTION

and

X 70480.

$$X = 10846.7177$$

### Figure 1

X. E. Chernikov

**X** **Chemical** **Formula** **Weight**

W. J. Sullivan, Jr., Director

Chapman, H. C. & J. A. M. 1993

Unidentified

X  
POLLUTION

N 78° 40' 8" E 6000 m

X  
C  
10-TAN 3003

10-JAN-2002. X

29-JUN 2001; 2001W0-EP07471

**X**



QY 332 CAAGCAAAATGCTTCTCAATCTAGATTCAACAATTAACAAGTTTGAGGCAAAATAA 391  
 DB 22045 AATTAATTTTCAAAATTTATTCCTTAAATATATAAACAATTAATATAATATAA 21986  
 QY 392 ACAATTTTGAAGATGAAGAAATCAAGAAATCAATTAATATAATATAA 430  
 DB 21985 CTAATTTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 21947

## RESULT 3

ABK31507:

ID ABK31507 standard; DNA: 38342 BP.

AC ABK31507:

DT 23-APR-2002 (first entry)

XX Signal transduction associated gene modified complementary DNA #175

XX Human: signal transduction associated gene; cytosine methylation state;

XX Type: island, signal transduction associated disease; solid tumour; cancer;

XX antitumour; cytostatic; mutant; ds.

XX Homo sapiens.

XX Synthetic.

XX OS

XX PN W0290200926-A2.

XX PD 03-JAN-2002.

XX PF 29-JUN-2001: 2001WG-EP07472.

XX PR 30-JUN-2000: 2000DE-1032529.

XX PS 01-SEP-2000: 2000DE-1043826.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A. Piepenbrock C, Berlin K;

XX PF WPI, 2002 147896/19.

XX PT Oligonucleotide for diagnosis and therapy of diseases associated with

XX signal transduction e.g. cancer, comprises chemically modified genomic

XX sequences of genes associated with signal transduction.

XX PS Claim 1: SEQ ID No 350; 24pp; English.

XX CC The present invention relates to chemically modified DNA sequences of

XX signal transduction associated genes. The DNA sequences are chemically

XX modified using a solution of bisulphite, hydrogen sulphide or

XX disulphite. Also disclosed are oligonucleotides and/or DNA oligomers

XX for detecting the cytosine methylation state (CG islands) of these

XX genes, and a method for the diagnosis and/or therapy of genetic and

XX epigenetic parameters of genes associated with signal transduction.

XX The genomic DNA can be obtained from cells or cellular components which

XX contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine,

XX cerebral-spinal fluid, tissue embedded in paraffin such as tissue from

XX eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver,

XX histologic object slides, and all their possible combinations. The

XX sequences of the invention are useful for the diagnosis and therapy of

XX diseases associated with signal transduction e.g. solid tumours and

XX cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA

XX sequences of different genes associated with signal transduction, or

XX their complementary sequences.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from the

XX European Patent Office.

XX SQ Sequence 38342 BP, 12471 A, 472 C, 7153 G, 18246 T; 0 other;

XX Query Match 10.1%; Score 51.4; DB 24.

XX Best Local Similarity 47.4%; Pred. No. 0.057;

XX Matches 189; Conservative 0; Mismatches 206; Indels 4; Gaps 1;

QY 36 ATTAAATGAATGTTTCAAGATGAAGAAATGAAGAAATGAAGAAATGAAGAAATGAAG 95  
 DB 22345 ATTAAATGAATGTTTCAAGATGAAGAAATGAAGAAATGAAGAAATGAAGAAATGAAG 22286  
 QY 96 TTTTATTTATTTATGAAGAAATGTTTCTTATATAGAGAGAGAGAGAGAGAGAGAGAG 156  
 DB 22285 TTTTATTTATTTATGAAGAAATGTTTCTTATATAGAGAGAGAGAGAGAGAGAGAGAG 22226  
 QY 156 TTTTATTTATTTATGAAGAAATGTTTCTTATATAGAGAGAGAGAGAGAGAGAGAGAG 215  
 DB 22225 TTTTATTTATTTATGAAGAAATGTTTCTTATATAGAGAGAGAGAGAGAGAGAGAGAG 22166  
 QY 216 AAG 275  
 DB 22165 AAG 22106  
 QY 276 AAG 331  
 DB 22105 AAG 22046  
 QY 332 GAAG 391  
 DB 22045 AATTAATTTTAAATTTATTTCTTAATATATAAATATATAATATATAATATAA 21986  
 QY 392 AGAATTTTCAATATGAGAAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430  
 DB 21985 CTAATTTTCTTAAATTTCTTAAATTTCTTAAATTTCTTAAATTTCTTAAATTTCTTAA 21947

## RESULT 4

ABK70514:

ID ABK70514 standard; DNA: 15674 BP.

AC ABK70514:

DT 01-JUL-2002 (first entry)

XX Chemically treated cell signalling 58A sequence complementary to 202.

XX Cell signalling: cytosine methylation; cell signalling disease;

XX cancer; cancer, cytostatic, ds.

XX Unidentified.

XX WS200202807-A2.

XX 10-JAN-2002.

XX 29-JUN-2001: 2001WG-EP07471.

XX 30-JUN-2000: 2000DE-1032529.

XX 01-SEP-2000: 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A. Piepenbrock C, Berlin K;

XX WPI, 2002 154755/20.

XX Nucleic acid, useful for diagnosis and therapy of diseases associated

XX with cell signalling e.g. cancer, comprises chemically modified genomic

XX sequences of genes associated with cell signalling

XX Claim 1: SEQ ID No 404; 24pp; sequence listing: English.

XX The invention relates to a nucleic acid comprising a sequence of at least

XX 18 bases of a segment of chemically pretreated DNA of genes associated

XX with cell signalling. The activity of the modified sequences of the

XX invention may be described as cytostatic. The object of the invention is

XX to provide the chemically modified DNA of genes associated with cell

XX signalling, as well as oligonucleotides and/or RNA-oligomers for

XX detecting cytosine methylations, as well as a method which is













PI diseases associated with DNA transcription, e.g. immunological  
PI disorders, Werner syndrome, psoriasis, myocardial infarction, solid  
PI tumours or cancer  
XX  
XX  
XX Claim 1: SEQ ID No 107; 32pp; English.  
XX  
XX the invention relates to a nucleic acid, which comprises a segment of the  
XX chemically pretreated DNA of genes associated with DNA transcription from  
XX one of 346 sequences, and an oligomer, in particular an oligonucleotide  
XX or peptide nucleic acid (PNA) oligomer that hybridises to or is identical  
XX to the chemically pretreated DNA of genes associated with DNA  
XX transcription. The set of oligomer probes are useful for detecting the  
XX expression of a gene, e.g. a disease-related gene, e.g. a gene, e.g. a  
XX in a chemically pretreated genomic DNA. The nucleic acids are useful for  
XX diagnosing or treating diseases associated with DNA transcription  
XX (particularly with the methylation of a gene) and a transgene expression  
XX deficiency, viral infection, retroviral infection, Scurvy syndrome,  
XX haematological disorders, immunological disorders, Werner syndrome,  
XX tuberculosis, developmental disorders, psoriasis, Kropfer's syndrome,  
XX neurological disorders, neurodegenerative disorders, Wardenburg  
XX syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial  
XX infarction, hypertension, aneuploidy, erythropoiesis, congenital heart  
XX disease, HIV syndrome, arthritis, polyinfarctum disorders, solid tumours  
XX or cancer. Sequences ABK28127-ABK28172 represent PNA transcription  
XX associated genomic DNA molecules of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format directly from the  
XX European Patent Office.

XX Sequence 15742 BP: 4638 A; 70 C; 2672 G; 8352 T; 0 other;

Query Match 9.6%; Score 48; DB 24; Length 15742;  
Best Local Similarity 50.3%; Prev. No. 0.29;  
Matches 144; Conservative 0; Mismatches 140; Indels 2; Gaps 1;  
QY 215 AAGGATAGGATATAAAATTTGGAAATCTTCAGAAACCAATGATATATATATATAAG 274  
II III III III III III III III III III III III III III III  
DB 14420 AAAATATTAAATATAAAATTTGAAAAATATAAAATATAAAATATAAAATATAAA 14361  
QY 275 AATAG 334  
II III III III III III III III III III III III III III III  
DB 14360 ATTAATATATATATATAAAATATAAAATATAAAATATAAAATATAAAATATAAA 14301  
QY 335 GGAATAG 394  
II III III III III III III III III III III III III III III  
DB 14300 AATTCAT 14243  
QY 345 ATTTTCAT 454  
II III III III III III III III III III III III III III III  
DB 14242 ATTTTCAT 14183  
QY 455 AAGGATAGGATATAAAATTTGGAAATCTTCAGAAACCAATGATATATATATATA 500  
II III III III III III III III III III III III III III III  
DB 14182 AATTCAT 14117

RESULT 15

ABL34175/c

ID ABL34175 standard; DNA; 113515 BP;

XX ABL34175;

XX 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID No: 2148.

XX Human; immune system disease; cytosine methylation; antiasthmatic;  
XX antiarteriosclerotic; antianemic; cytosine; neuroprotection;  
XX neuroprotection; anti-HIV; antineoplastic; ophthalmological;  
XX antirheumatic; antirheumatic; antidiabetic; antipsoriasis;  
XX antineoplastic; cancer; eye disease; arteriosclerosis; aneuploidy;  
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

KW gene; ds.

XX Homo sapiens.

XX WO2002/00928-A2.

XX 04-JAN-2002.

XX 02-JUL-2001: 2001WO-EP07547.

XX 20-JUN-2002: 2002DE-1032529.

XX 01-SEP-2000: 2000DE-1043826.

XX (EP16) EP-DE-9105 AG.

XX 01-JAN-2002: 2002DE-1032529.

XX 01-JAN-2002: 2002DE-1032529.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
XX for diagnosis and treatment of diseases associated with abnormal  
XX cytosine methylation -

XX Claim 1, SEQ ID NO 2142, 32pp - Sequence Listing; German.

XX The present invention provides a number of human immune system associated  
XX genes which are modified by the methylation of cytosines. The sequences  
XX including eye diseases such as retinopathy, neovascular glaucoma and  
XX macular degeneration, arteriosclerosis, aneuploidy, cancer, acute myeloid  
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
XX rheumatoid arthritis, psoriasis and inflammatory/immune bowel  
XX diseases. The present sequence is a gene of the invention.

XX Sequence 113515 BP: 35172 A; 1174 G; 22520 C; 54649 T; 0 other;

Query Match 9.6%; Score 48; DB 24; Length 113515;  
Best Local Similarity 47.8%; Prev. No. 0.17;

Matches 141; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 96 TTTTATTTTATAGAAAATGCTCTCTATAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 156  
II III III III III III III III III III III III III III III

DB 40687 TTTTATTTTATAGAAAATGCTCTCTATAGAAAGAAAGAAAGAAAGAAAGAAAG 40628  
II III III III III III III III III III III III III III III

QY 156 CTCTCAGCTCAGTATGATGATTTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 215  
II III III III III III III III III III III III III III III

DB 30627 ACATTCGATCTTATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTT 40568  
II III III III III III III III III III III III III III III

QY 216 AAGGATAGGATATAAAATTTGGAAATCTTCAGAAACCAATGATATATATATATAAG 275  
II III III III III III III III III III III III III III III

DB 40567 AAT 40509  
II III III III III III III III III III III III III III III

QY 276 AAT 335  
II III III III III III III III III III III III III III III

DB 30507 TTTATCTTCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC 40448  
II III III III III III III III III III III III III III III

QY 336 GAAATAGCTTCTGATCTAGAAATTTCAAAATTAATTAATTAATTAATTAATTAATTA 391  
II III III III III III III III III III III III III III III

DB 40447 ACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 40392  
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Search completed: January 4, 2003, 15:08:49  
Job time : 252.507 secs







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CNS020K7/
LOCUS       1502 bp            linear            GSS 12 MAY 2000
DEFINITION Tetradon nigroviridis genome survey sequence 17 end of clone
22111 of library 6 from Tetradon nigroviridis, genome survey
sequence.
ACCESSION   AL175696.1   GI:7814753
VERSION     AL175696.1
KEYWORDS    GSS: genome survey sequence;
SOURCE      Tetradon nigroviridis;
ORGANISM    Tetradon nigroviridis;
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Tetraodon; Euteleostei; Neoteleostei;
            Acanthopterygii; Perciformes; Tetraodontiformes;
            Tetraodontidae; Tetradon;
            1 (bases 1 to 1092)
REFERENCE   1 (bases 1 to 1092)
AUTHORS    Roest-Crollius,H.; Jallion,G.; Basille,C.; Bouneau,L.; Fisher,C.;
            Kerpet,A.; Frazzetta,C.; Winkler,P.; Rattier,P.; Quetier,F.;
            Samin,W.; and Weissbach,J.
TITLE      Human gene number estimate provided by genome wide analysis using
            tetradon nigroviridis DNA sequence
JOURNAL     unpublished
AUTHORS     Roest-Crollius,H.; Jallion,G.; Basille,C.; Frazzetta,C.; Fisher,C.;
            Bouneau,L.; Winkler,P.; Kerpet,A.; Rattier,P.; Quetier,F.;
            and Weissbach,J.
TITLE      Freshwater pufferfish Tetradon nigroviridis
JOURNAL     unpublished
REFERENCE   2 (bases 1 to 1092)
AUTHORS    Roest-Crollius,H.; Jallion,G.; Basille,C.; Frazzetta,C.; Fisher,C.;
            Bouneau,L.; Winkler,P.; Kerpet,A.; Rattier,P.; Quetier,F.;
            and Weissbach,J.
TITLE      Freshwater pufferfish Tetradon nigroviridis
JOURNAL     unpublished
REFERENCE   3 (bases 1 to 1092)
AUTHORS    Roest-Crollius,H.; Jallion,G.; Basille,C.; Frazzetta,C.; Fisher,C.;
            Bouneau,L.; Winkler,P.; Kerpet,A.; Rattier,P.; Quetier,F.;
            and Weissbach,J.
TITLE      Freshwater pufferfish Tetradon nigroviridis
JOURNAL     unpublished
COMMENT     Direct Submission
            Submitted (12 APR 2000)
            this sequence is a single read and was generated as part of a large
            scale clone-and-sequencing project of the Tetradon nigroviridis
            genome. For more information please take a look at
            http://www.genoscope.cns.fr/brun-14
FEATURES             Location/Qualifiers
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                         1..1092
                         /organism="Tetradon nigroviridis"
                         /db_xref="taxon:7227"
                         /clone_lib="RPCI-98"
                         /note="end : 17"
BASE COUNT      48 a 169 c 165 g 262 t 119 others
ORIGIN
Query Match      10.7%; Score 52.4; DB 17; Length 1092;
Best Local Similarity 35.0%; Pred. No. 0.17; Labels 0; Gaps 0;
Matches 147; Conservative 67; Mismatches 189;
QY 50 ATATTTTAACTGAGTACTTAATTAACAATTAACTATGTTGTTTAAAGTGGCTGTA 109
DB 1003 ATTTTTTTTTTTAAATAAATAAATAAATTTTNTTTTAAATTTTTTTTTTTT 944
QY 110 GAAAAATTCAGACAGAGAGTAGACACACATTAAGCTTTTCATGTAATAATTTGAGT 169
DB 943 WAAAAAATAAAAAAATAAAAAAATAAAATTAATAAAAAAATAAAATTTTAAAT 884
QY 170 TTAATTTTAACTGAGTCTTTGGGAGCTGCTGCAATTAATTAAGCTTATGCTACACAAA 229
DB 883 TTTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 824
QY 240 TGGGAGCTTGAAAAGAGGCTGATGACATAATTAATTAATTAAGTACGCAAAATTTGAA 289
DB 823 AAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 764
QY 290 GTATGATATGAATACATATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 349
DB 763 WTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 704
QY 450 AATTTTTCAGAGTAGATATATATATATATATATATATATATATATATATATATATAT 409
DB 703 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 544

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QY 410 TACGATTTTATATAATAAT 426
DB 643 TTTTTTTTTTTTTTWWWW 627

RESIDU 6
CNS000VL
CNS000VL
DEFINITION 1101 bp            linear            GSS 04 JUN 1999
            Drosophila melanogaster genome survey sequence 77 end of BAC
            BAC29021 of RPC1-98 library from Drosophila melanogaster (fruit
            fly), genome survey sequence.
ACCESSION   AL069706.1   GI:4949849
VERSION     AL069706.1
KEYWORDS    GSS;
SOURCE      Drosophila melanogaster;
            ORGANISM    Drosophila melanogaster;
            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila;
            1 (bases 1 to 1101)
REFERENCE   1 (bases 1 to 1101)
AUTHORS    Genoscope;
            DIRECT SUBMISSION
            Submitted (02 JUN 1999) Genoscope Centre National de Sequencage
            BP 191 91006 Evry cedex - FRANCE (E-mail : seqret.genoscope.cns.fr
            Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see: http://www.fruitfly.org/TheBDGP/Drosophila
            melanogaster/BAC library was prepared by Kazuo Osoegawa and
            Aurea Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPC1-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
            c1 and k1 libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BAC Resource Center can be
            found at: http://www.fruitfly.org/BAC/drosophila_bac.htm.
            Location/Qualifiers
                     1..1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPC1-98"
                     /note="end : 17"
BASE COUNT      419 a 91 c 60 g 299 t 212 others
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Best Local Similarity 30.8%; Pred. No. 0.25; Labels 0; Gaps 0;
Matches 147; Conservative 87; Mismatches 244;
QY 24 CTGTTACTTTCATATGAGTGAAGAGAAATATTTTAACTTAACTATTTATTTAAAT 82
DB 454 YTTTCATTTTMMMMWAAATTTTAAATAAAATTTAAATTTTAAATTTTAAATTTT 514
QY 83 TAAGTATGTTTAAAGTGGCTGTAGCAAAATTTACATAGAAAGAGTACACACAT 142
DB 514 WWWTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 574
QY 143 TAAATTTTACATATAAATTTTGTGATGTTCTATTTTAACTCAATTTTGGTATGTT 202
DB 574 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 634
QY 203 AAATAATTAAGTATATCTTCCACAAATGGGTGGCTTGAAGAAAGGCTATGATATA 262
DB 634 TTAATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 694
QY 263 ATTATATCTTTAGCGCAAAATTTGTAATGTTATGTAATGTAATGTAATGTAATTT 322

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Db 694 AAAAAAAAAAAATWAAWAAATWATAWATAWTTAAAAWAAATAAAWAAWAAATWAAWATA 753
QY 723 GGAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 382
Db 754 ATATWATAATATWTTWAAWAAATWAAWAAATWAAWAAATWAAWAAATWAAWAAATWAAW 813
QY 783 ACATACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTAC 442
Db 814 TATATWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 873
QY 443 GGAGACTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499
Db 874 AAAAAATAAWTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 930

RESULT 7
CN50124K
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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location/Qualifiers
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/plasmid="pBelobAC11"
/notes="end : T7"

BASE COUNT 401 a 97 c 116 g 136 t 335 others

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Best Local Similarity 26.84; Score 52.8; DB 17; Length 1085;
Matches 84; Conservative 93; Mismatches 137; Indels 0; Gaps 0;

QY 1 ATGTGGGAATTTATCATCAGCTTACTTTCATATGAGTCAAGTCAAGTCAAGTCAAGTCAAG 60
Db 726 AAKTAKRTAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 785
QY 61 CTCAGTAGTTTAAATTTACAAATTTAAGTATGTGTTTAACTGCTGCTTACGAGAAATTTCA 120
Db 786 KAAATKTTTATKRTKIDIAKTTAAKATTTKATTTKTTDKKAAKAAKAAKAAKAAKAAK 845
QY 121 CTAGAGAGTAGTGAAGACACTTAAAGTTTTCATGTAAATTTTGTGAGTCTTATTTTAA 180
Db 846 KAKKAKKKTAKKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 905
QY 181 CTGATCTTTTGGCATCTGTCGACAAATTAACGTTATGCTTACCAAAATGCTGTGCTT 240
Db 906 AAKTTTFFFTTATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 965

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QY 241 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 300
Db 266 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 365
QY 301 GAATACATATCAT 314
Db 1026 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1085

RESULT 8
CN501K83/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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location/Qualifiers
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/plasmid="pBelobAC11"
/notes="end : Sp6"

BASE COUNT 312 a 138 c 89 g 255 t 41 others

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Matches 139; Conservative 17; Mismatches 162; Indels 0; Gaps 0;

QY 2 TGTGCGAATTTATCATCAGCTTACTTTCATATGAGTCAAGTCAAGTCAAGTCAAGTCAAG 61
Db 458 TGTGCGAATTTTGTGCGAATTTTGTGCGAATTTTGTGCGAATTTTGTGCGAATTTTGTGCG 299
QY 62 TCAATAGTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 121
Db 258 TCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 249
QY 122 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 181
Db 238 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 179
QY 192 TCAATTTTGTGCGAATTTGTGCGAATTTGTGCGAATTTGTGCGAATTTGTGCGAATTTGT 241
Db 179 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 119
QY 242 AAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 301
Db 118 AAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 59

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Db 719 ATATKAGKGCCTTTTITTTTWWAWANAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 778
QY 144 AAGATTTTCAAGTAAATTTGAGTGTCTATTTTAACTGAGTGTCTGCACTGTGCA 203
Db 779 AWAATWAKTATGATAAAIAWAAATTTTWTATTTTAAATTTTAAATTTTAAATTTTAAATTT 848
QY 204 AAGATTTTCAAGTAAATTTGAGTGTCTATTTTAACTGAGTGTCTGCACTGTGCA 263
Db 839 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 898
QY 254 ATACAGTGTCTAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCT 923
Db 899 ATTTTITTTTITTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 958
QY 324 CACAAGTGTCTAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCT 983
Db 959 TAAATWAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1018
QY 384 CAGTTACCTAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCT 443
Db 1019 TAAATWAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1078
QY 444 GAGAGTAAATGAAGA 459
Db 1079 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1094

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RESULT 11
CNS015LM/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of PAC
BACN14105 of Drosophila library from Drosophila melanogaster (fruit
fly); genomic survey sequence.
ACCESSION
AL105604.1 GI:5617618
VERSION
1
KEYWORDS
GSS.
ORGANISM
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydridea; Drosophilidae; Drosophila.
Genoscope.
REFERENCE
1 (bases 1 to 1061)
AUTHORS
Direct Submission
SUBMITTER
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this PAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (DGP) -
http://www.dgp.ebi.ac.uk - this Drosophila melanogaster PAC
library (Dros PAC) was made by Alain Billaut at CERF (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Richeton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.
FEATURES
Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN14105"
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/note="end : T7"
BASE COUNT
342 a 138 c 89 g 277 t 215 others
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Best Local Similarity 34.9%; Pred. No. 0.79;
Matches 156; Conservative 67; Mismatches 222; Indels 2; Gaps 1;
QY 30 TTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 89
Db 1061 TTTTITTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1002

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RESULT 12
CNS015M/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET2 end of BAC;
BAC29490 of RPCL-98 library from Drosophila melanogaster (fruit
fly); genomic survey sequence.
ACCESSION
AL069440.1 GI:4549583
VERSION
1
KEYWORDS
GSS.
ORGANISM
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydridea; Drosophilidae; Drosophila.
Genoscope.
REFERENCE
1 (bases 1 to 1101)
AUTHORS
Direct Submission
SUBMITTER
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BAC is constructed a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.flybase.org The BDGP Drosophila
melanogaster BAC library was prepared by Karotzko, Osada and
Aaron Mammeter in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; on the sp. the same strain used for the BACs
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://www.flybase.org/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BAC29490"
/clone_lib="RPCL-98"
/note="end : TET3"
BASE COUNT
406 a 66 c 104 g 351 t 214 others

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## : TITLE OF INVENTION: SAME AND METHODS OF USE

: FILE REFERENCE: S01P1300-3

: CURRENT APPLICATION NUMBER: US/09/764,855

: PRIOR FILING DATE: 2001-08-24

: PRIOR APPLICATION NUMBER: US 60/227,866

: PRIOR FILING DATE: 2000-08-24

: PRIOR APPLICATION NUMBER: US 60/264,647

: PRIOR FILING DATE: 2001-01-16

: PRIOR APPLICATION NUMBER: US 60/300,111

: PRIOR FILING DATE: 2001-06-22

: NUMBER OF SEQ ID NOS: 5379

: SEQ ID NO 5027

: LENGTH: 2000

: TYPE: DNA

: ORGANISM: Arabidopsis thaliana

US-09-764-855-180

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Best Local Similarity 50.4%; Pred. No. 22;  
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 47 AATAATTTTAAACATCACTTTAAATTAACATTTAAGTATGCTTTTAAAGTGGCTG 106

DB 447 ATAAAAATGAAAAATATAAATAATTTTCAAAATAAATATAAATATAATGACG 288

QY 107 TTAGTAAAAATTCAGTAAAGATGTATAGATATTAAGATTTTCAAGTAAATTTG 106

DB 287 TAGAAAAAATATCAAAATAAGCTGACGTTAAAAATTTTAAATTAATATATATT 228

QY 167 AGTCTATTTTAAACGAAATCTTTTGGATGCTGCAAAATAATTAAGCTATATCTTC 228

DB 227 TAATTTTTTTTCTGTTAATCTGATCAAAATTTGGTAAAGAAATAATTTTCTAC 171

## RESULT 15

US-09-764-855-180

: Sequence 180; Application US/09/764,855

: Patent No. US2002/119519A1

: GENERAL INFORMATION:

: APPLICANT: Rosen et al.

: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

: FILE REFERENCE: P110

: CURRENT APPLICATION NUMBER: US/09/764,855

: PRIOR FILING DATE: 2001-01-17

: PRIOR application data removed - consult P110 or file wrapper

: NUMBER OF SEQ ID NOS: 534

: SOFTWARE: Patent In Ver. 2.0

: SEQ ID NO 180

: LENGTH: 3785

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-764-855-180

Query Match 7.2% Score 66.2; DB 10; Length 3785;  
Best Local Similarity 51.6%; Pred. No. 25;  
Matches 83; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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DB 507 TAAAAATTAAGTAAAGTAAATCTTAAATTAATTAATTAATTAATTAATTAATTC 566

QY 318 TTAGAGAAAGAGTTGATATTTATTAAGAAATCTTCAAAAGTATAGTAAATATTC 477

DB 567 TGTAGAAATAGAGTTTATAGAAATTAAGAGTCTGAGAAATAAGTATATATTT 626

QY 378 ATGATACATCTAGATGATCATGAAATTTGACACTTT 418

DB 627 AGAAGAGCTCTTTAAAGAGTATGATTTGAGACTGT 667

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Job time : 982.486 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 4, 2002, 10:57:01 ; Search time 1074.726 seconds  
(without alignments)  
10282.476 Million cell updates/sec

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Scoring table: `IDENTITY_NGC`  
Gapop 10.0 , Gapext 1.0

Searched. 3185235 seqs, 112999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                  Listing first 45

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

result No.	Score	%		Length	DB	ID	Description
		Query	Match				
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2	52.6	10.5	11049	24	ABL49421		Human polynucleoti
3	52.6	10.5	11049	24	ABL3266P		Human immune syste
4	48.2	9.6	6077	24	ABL3246P		Human immune syste
5	45.8	9.1	14924	24	ABL934322		Chemically treated
6	45.8	9.1	14924	24	ABL336255		Human immune syste
7	45.6	9.1	8467	24	ABL432108		Human immune syste
8	45.6	9.1	11036	22	AKS45411		Chemically pretrea
9	45.6	9.1	11036	24	AKR28264		DNA transcription

[illegible]































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? APPLICANT: Mohr, Christine
? APPLICANT: Wendland, Jürgen
? APPLICANT: Knechtle, Philipp
? APPLICANT: Reibschung, Corinne
? TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYYP11
? TITLE OF INVENTION: AND USES THEREOF
? NUMBER OF SEQUENCES: 1152
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 6239264artis Corporation
? STREET: 3034 Cornwallis Road
? CITY: Research Triangle Park
? STATE: No. 6239264th Carolina
? COUNTRY: USA
? ZIP: 27709
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-Dos/MS-Dos
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/88/598.416
? FILING DATE: 24-DEC-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: CH 0016/97
? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/CHECK: NMEFF#F 5-2020-A 000177
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 919-541-8587
? TELEFAX: 919-541-8689
? INFORMATION FOR SEQ ID NO: 535:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 827 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
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? ORIGINAL SOURCE:
? ORGANISM: PAGI373RP
? US-08-998-416-535

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Query Match  
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QY	69	TTTAATTACAATTAAGTAGTGTTTAAAAGTGCGCTGGTASCAAALPACHAACAGS	128
Dd	355	TATATAATTAAATATATANAATTTTAAATTACITCATCATATATATATATTAAAA	414
QY	129	ANGTAGCACACAGCTAAGTTTCATGTAAAAATGGAGLICTATTTTIACTGAATCT	188
Dd	415	TGTACSHICAAALAIFUAITTATTATGCTAGTAATAATCTTATTTAATAGTCTGCC	474
QY	189	TTIGSCAUGTGCTAACAAATTAGCTTCCCTTCACAAAAGSGGCGCTTGA AAAAGG	248
Dd	475	TTTAATGGATATTACIACCTACTAAATATTTTACCFAATAATATATTATTAAGAAT	534
QY	249	CCTGATGCAATAATATTACAGTTGTAGAGAAATTTGAATGTTATCATATATGAATAC	308
Dd	535	AAATCAATAATTATATATCACTAAAGTATATAAAATTAATTAATCTTTTAAATTAT	594
QY	309	ATTCATTTTTACGGGAAGAGGCTTGSAATTTTATCAACAATAATCTTTTAAATTA	368
Dd	595	AATCATATAATAAGAGAAATATAATATTATTATTAAAGATAATTTTGTATAATAATA	654
YY	369	I AAU CAUT CAT GT AT C AC TT ACC TAG TG CT CAT GA AAT TTT 409	

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QY 250 GCGATCGATAAATATTTAATAGTTGTAAGGCACAAAATTTGTAATGCTATGTAATGCAATACATA 309
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 515 TTCTGCTTTCTCAATTTAATATAAATATATATATATATATATATATATATATATATATATAT 456
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 410 TTGATTTT 417
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DB 455 TTGATTTT 448
    | | | | |

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Search completed: January 4, 2003, 15:14:01  
Job time : 79.9648 secs













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: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 2378..5038
: FEATURE:
: NAME/KEY: CUS
: LOCATION: 2378..5038
:
US-07 867-106-2

```

```

Query Match
Best Local Similarity 49.5%; Pred. No. 3.3; Length 5852;
Matches 94; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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QY 247 ATACACTACCCAGTAGTGTGAGACACATTTTAAAGAAATGAGGAGAACT 306
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2124 ATACCTATTATAAFAATGGAATATATATATATATATATATATATATAT 2183
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 GTCATTGCTATATCTTTATGATATATATATATATATATATATATATAT 366
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2184 TTTAATATATATATATATATATATATATATATATATATATATATAT 2243
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 AAGCAATATATATATATATATATATATATATATATATATATATATAT 426
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2244 TTTTATATATATATATATATATATATATATATATATATATATATAT 2303
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 TAAATATATATATATATATATATATATATATATATATATATATAT 2303
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2304 TAAATATATATATATATATATATATATATATATATATATATATAT 2313
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 13
US-09-134-001C-210/C
: Sequence 210; Application US/09134001C
: Patent No. 6380370
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
: FILE REFERENCE: GPC-007
: CURRENT APPLICATION NUMBER: US/09/134,001C
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 210
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Staphylococcus epidermidis
US-09-134-001C-210

```

```

Query Match
Best Local Similarity 58.3%; Pred. No. 2.8;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```

```

QY 306 TGTGATTGCTATATCTTTATGATATATATATATATATATATATATATAT 365
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Db 584 TGTGTTTACTATTTTAAATGAGGATATATATATATATATATATATATATAT 525
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 366 AAGTACATTTGATTTTATTTTATATATATATATATATATATATATATAT 413
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 AATTGCTTTTATCTTTGATATGCTTTTGTACITTTTCTTCTGCA 477
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 14
US-08-998-416-786
: Sequence 786; Application US/08998416
: Patent No. 629264

```

```

: GENERAL INFORMATION:
: APPLICANT: Philippsen, Peter
: APPLICANT: Kohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christine
: APPLICANT: Wendland, Jürgen
: APPLICANT: Knechtle, Philipp
: APPLICANT: Reibschuh, Corinne
: TITLE OF INVENTION: SYNTHETIC LNA SEQUENCES OF ASHWA GOSYPHII
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 629264artis Corporation
: STREET: 3054 Gornwallis Road
: CITY: Research Triangle Park
: STATE: No. 629264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/998,416
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Melius, Timothy
: REGISTRATION NUMBER: 38,241
: PREFERRED OFFICE: RPOFFICE
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-9897
: TELEFAX: 919-541-9889
: INFORMATION FOR SEQ ID NO: 786:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 711 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: FAG1504UP
: US-08-998-416-786

```

```

Query Match
Best Local Similarity 52.6%; Pred. No. 2.8;
Matches 75; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

```

```

QY 252 CTATCCATATCTTTGATAATTTTATTTTATTTTATTTTATTTTATTTT 311
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 CTATTAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 355
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 912 TTTGATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 371
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 CTAAATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 415
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 372 CATTTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 391
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 AATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 435
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 15
US-08-204-675-1
: Sequence 1; Application US/08204675
: Patent No. 5677170
: GENERAL INFORMATION:
: APPLICANT: Levine, Scott E.
: APPLICANT: Becker, Joel D.
: APPLICANT: Braiterman, Leifila T.

```



GenCore version 5.1.1  
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OM nucleotide - nucleotide search, using sw model  
Run on: January 7, 2003, 11:04:05, Search time 28.4855 seconds  
(without alignments)  
7606.585 Million cell updates/sec

Title: US-09-776-705-3\_COPY\_30000\_30500  
Perfect score: 501  
Sequence: 1 aatgaatttttttaaaatqt.....ataatgatctatctacaat 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 / Gapext 1.0

Searched: 481593 seqs, 216252194 residues  
Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published\_Applications\_NA:\*

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2	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
3	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
4	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
5	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
6	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
7	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
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9	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
10	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
11	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
12	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
13	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
14	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	501	100.0	3768	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
4	501	100.0	42373	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
5	249.6	47.8	395	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
6	240.8	45.1	455	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
7	177	35.4	4857	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
8	54.8	10.9	363	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
9	45.6	9.1	479	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
10	44.2	8.8	377	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
11	44.2	8.8	3876	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
12	41.2	8.2	426	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
13	41.2	8.2	426	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
14	40.4	8.1	355	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
15	40.4	8.1	390	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
16	40.4	8.1	413	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
17	40.4	8.1	425	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
18	39.5	7.9	428	US-09-776-705-3_COPY_30000_30500	Sequence 28, Appl
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US-09-776-705-3\_COPY\_30000\_30500

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us-09-776-705-3\_copy\_30000\_30500.rnpb

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